Anti-Nogo TSH recep TSH recep Humanised Anti-huma Anti-huma

Anti-huma Human 149 Human 149 Human 149

Adm31981 Abp96777 Abp96778 Aay80284 Aaw71876 Aaw71876 Adp48650 Adp48657 Adp48657 Adp48657 Adp48657 Adp48657 Adp48657 Adp48658 Adp48658 Adp48658 Adp48658 Adp48658 Adp48658 Adp48658 Adp48658 Adp48658

ADM33991 ABP96777 ABP96777 AAY1876 AAW11876 AAW12918 AAW12918 ADP48666 ADP48665 ADP4866 ADP486 A

219 219 2239 2239 2251 2251 2251 2251 612 612

Human L49 Human L49 Fusion pr

Human Human Human

```
Addy2966 Humanised Addy2860 Humanised Adgy2860 Humanised Aae27852 Murine mo Aae27854 Murine mo Aae27854 Murine at Aae27854 Muse 14. Addy7256 Humanised Aav76126 Humanised Aav76126 Humanised Aav76126 Humanised Aav76126 Humanised Aav76136 Humanised Aav76136 Humanised Aav76136 Humanised Aav76136 Humanised Aav76136 Humanised Aav76136 Humanised Addy25716 Humanised Addy25716 Humanised Addy25716 Humanised Addy2716 Humanised Addy271877 Atti-huma Aav1877 Atti-huma Aab12914 Anti-huma Aab12914 Anti-dans Aar72599 Anti-dans
                                                          April 18, 2005, 09:41:10 ; Search time 62 Seconds (without alignments) 704.902 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                     US-10-737-208A-1
595
1 DVVMTQTPLSLPVTPGEPAS......SQSTHVPPLTFGAGTKLELK
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                               2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP42956
ADP42956
ADP42956
ADG27856
ADG67228
AAR11598
AAR27864
AAR27864
AAR27864
AAR27864
AAR27864
AAR31063
AAR31046
AAW36450
AAY50733
AAR31046
AAW36450
                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                   A_Geneseq_16Dec04:*
11: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2002s:*
7: geneseqp2003ss:*
8: geneseqp2003ss:*
                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *
Query
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                        OM protein
                                                                                                                             Sequence:
                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                       Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.18
```

Ur region

Pred.

Local Similarity

N

```
ö
           The invention relates to a novel antibody variable region, where the antibody variable region specifically binds to human cell surface glycosphingolipid GD2. An antibody variable region of the invention has cytostatic activity, and may have a use in gene therapy. The antibody may be used for treating cancer. The nucleic acid or cell is useful for manufacturing a medicament that may be used for treating diseases such as cancer. The present sequence represents humanised immunoglobulin light humanised immunoglobulin light
                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New modified m14.18 antibodies with reduced immunogenicity and that specifically bind the human cell surface glycosphingolipid GD2, useful for treating cancer.
                                                                                                                                                                                                                                         DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                   SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                 immunoglobulin; antibody; GD2; cytostatic; gene therapy; cancer; cell surface glycosphingolipid.
                                                                                                                                                                                         .
0
                                                                                                                                                                Length 113;
                                                                                                                                                                                        Indels
                                                                                                                                                            ; Score 595; DB 8;
; Pred. No. 1.3e-43;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO:5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 5; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised immunoglobulin light chain
                                                                                                                                                                                                                                                                                                                                                                 Ŕ
                                                                                                                                                                                                                                                                                                                                                              ADP42960 standard; protein; 220
                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-DEC-2003; 2003WO-EP014295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-DEC-2002; 2002US-0433945P
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-488049/46.
N-PSDB; ADP42959.
                                                                                                                                                                        Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ъ
К;
                                                                                                                                    Sequence 113 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004055056-A1
                                                                                                                                                                                                                                                                                                                                                                                                                   23-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gillies SD,
                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                         ADP42960;
                                                                                                                                                                                                                                                                                                                                                ADP42960
요
                                                                                                                                                                                                                                                                                            g
G
                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                     ò
```

The invention relates to a novel antibody variable region, where the antibody variable region specifically binds to human cell surface glycosphingolipid GD2. An antibody variable region of the invention has cytostatic activity, and may have a use in gene therapy. The antibody may be used for treating cancer. The nucleic acid or cell is useful for manufacturing a medicament that may be used for treating diseases such as cancer. The present sequence represents humanised immunoglobulin light

Length 220;

100.0%; Score 595; DB 8;

Sequence 220 AA;

Query Match

```
9
                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an immunogenically modified fusion protein derived from a parent fusion protein, comprising first and second proteins/polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is an immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in combining known favourable properties of a composition or in creating new properties of a composition which elicits biological or pharmacological efficacy without having undesirable physiological effects such as nausea or gastric upset. The present sequence is mouse 14.18 antibody modified epitope. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                     Mouse; fusion protein; immunological; major histocompatability complex; MHC; gastric upset; nausea; 14.18 antibody.
                                                                             1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                       61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New modified fusion protein with reduced immunogenicity, useful combining favorable properties of a composition, comprises an immunoglobulin molecule linked to a non-immunoglobulin target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 113;
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 570; DB 5; Length 11
Pred. No. 1.8e-41;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hamilton A,
              red. No. 2.4e-43;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carter G,
Way JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 19; Page 78; 92pp; English.
                                                                                                                                                                                                                              AAE27856 standard; protein; 113 AA
                                                                                                                                                                                                                                                                                                                        VK region #2.
'0
ਪਾਰ '80.001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones T,
Baker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-FEB-2001; 2001EP-00103955.
05-APR-2001; 2001EP-00108291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-2002; 2002WO-EP001690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.8%;
96.5%;
                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 96.5
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carr FJ,
Watkins J,
                                                                                                                                                                                                                                                                                                                        antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-667054/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               WO200266514-A2.
                                                                                                                                                                                                                                                                                         13-DEC-2002
                                                                                                                                                                                                                                                                                                                        Mouse 14.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide.
                            113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gillies S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanlon M,
                                                                                                                                                                                                                                                            AAE27856;
                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                  Mus sp.
            Best Loca
Matches
                                                                                                                                                                                              RESULT 3
AAE27856
                                                                                     셤
                                                                                                                       ò
                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113

19

셤

```
ò
                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (MHC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful tor preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically nonmodified biological molecule identified is useful for preparing a biological molecule with reduced immunogenicity and having a retained desired biological activity, where the T-cell epitope is a lamer peptide. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide
                                                                                                                                                                                                                 human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hamilton A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.8%; Score 570; DB 5; L 96.5%; Pred. No. 1.8e-41; iive 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams S,
                                                                                                                                                                                       14.18 antibody VK mouse modified epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 21; Page 67; 85pp; English
                                                                                            A
                                                                                           ADG67528 standard; protein; 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001EP-00110220.
2001EP-00113228.
2001EP-00124965.
2001EP-00126859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001EP-00106899.
2001EP-00107012.
2001EP-00107568.
                                                                                                                                                                                                                                                                                                                                                                                                          2001EP-00105777
2001EP-00106536
                                                                                                                                                                                                                                                                                                                                                             18-FEB-2002; 2002WO-EP001688
                                                                                                                                                                                                                                                                                                                                                                                                                                         2001EP-00106538
                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MERE ) MERCK PATENT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to MHC molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carter G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-750424/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 113 AA;
                                                                                                                                                                                                                                                                                                 WO200269232-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAR-2001;
27-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                             19-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-2001;
15-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2001;
20-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-2001;
                                                                                                                                                        11-MAR-2004
                                                                                                                                                                                                                                                                                                                                06-SEP-2002
                 61
                                                                                                                           ADG67528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carr FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binding
                                                                                                                                                                                                                                                                    Мив вр
```

```
Two separate H and L chain cDNA libraries were prepared from mRNA isolated from the murine hybridoma cell line 14.18. The lambda gilo library was enriched for full-length L- and H-chains. It was screened by filter hybridisation using various C region probes. Ten phage clones from each screening were analysed further by restriction analysis. The L chain CDNA sequence was sequenced and the amino acid sequence deduced from it. It appears to include a 19 amino acid leader followed by sequences that are highly homologous to the anti- GAI family of V(kappa) genes. See also AAQ11291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prodn. - e.g. having dual biological activity, esp. transfecting host cell with constructed cassette and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                chimaeric binding protein; immunoglobulin; variable region; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.8%; Score 570; DB 2; Length 150; 96.5%; Pred. No. 2.3e-41; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                       Murine monoclonal 14.18 L chain V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133. .151
/label= kappa C region
                                                                                                                                                                                                                                                                                                                                                                                                                              1. .19
/label= leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                         Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121. .132
/label= J(kappa5)
                                                                                                                         AAR11598 standard; protein; 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Fig 3; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89US-00409889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89US-00409889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 96.5
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibodies, by trans
second DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-117518/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ11292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 150 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ABBO ) ABBOTT
                                                                                                                                                                                                             14-JUN-1991
                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-APR-1991.
                                                                                                                                                                                                                                                                                                                         light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9104329-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gillies SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                  AAR11598;
               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

ö

ô

ö

Indels

Conservative

Best Local Similarity Matches 109; Conserv

н

δ

9 9

DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF

AAE27854 RESULT

g

Mus sp.

```
The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (WHC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful tor preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically nonmodified biological molecule with reduced immunogenicity and having a retained biological molecule with where the T-cell epitope desired biological activity, where the T-cell epitope is a lamer peptide. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                      human, mouse, T-cell epitope, major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide binding to MHC molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVPDRFSGSGSGTDFTLKISRVEAEDSGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                 14.18 antibody VK mouse peptide threaded modified epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hamilton A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.8%; Score 558; DB 5; 94.7%; Pred. No. 1.9e-40; iive 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 21; Page 67; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB21363 standard; protein; 114 AA
                                                                                                                                                                                                                                                                                                                                                             08-MAR-2001; 2001EP-00105777.
15-MAR-2001; 2001EP-00106536.
15-MAR-2001; 2001EP-00106538.
20-MAR-2001; 2001EP-00106899.
20-MAR-2001; 2001EP-00107012.
27-MAR-2001; 2001EP-00107568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jones T,
                                                                                                                                                                                                                                                                                                  18-FEB-2002; 2002WO-EP001688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2001; 2001EP-00110220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2001; 2001EP-00113228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-OCT-2001; 2001EP-00124965.
12-NOV-2001; 2001EP-00126859.
                        11-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERE ) MERCK PATENT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 94.7°
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carr FJ, Carter G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-750424/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 113 AA;
                                                                                                                                                                                                               WO200269232-A2.
                                                                                                                                                                                                                                                                                                                                            19-FEB-2001;
                                                                                                                                                                                                                                                           06-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                          Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB21363
ID AAB2
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an immunogenically modified fusion protein derived from a parent fusion protein, comprising first and second proteins/polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is non-immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in combining known favourable properties of a composition or in creating new properties of a composition which elicits biological or pharmacological effects such as nauses or gastric upset. The present sequence is mouse 14.18 antibody modified epitope. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DVVMIQIPGSLPVSAGDQASISCRSSQSLVHRNGNIYLHWYLQKPGOSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                          Mouse; fusion protein; immunological; major histocompatability complex; MHC; gastric upset; nausea; 14.18 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New modified fusion protein with reduced immunogenicity, useful for combining favorable properties of a composition, comprises an immunoglobulin molecule linked to a non-immunoglobulin target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 558; DB 5; Length 11 Pred. No. 1.9e-40; 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hamilton A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carter G,
Way JC;
                                                                                                           Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 19; Page 78; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ą.
                                                                                                                                                                                                                               Mouse 14.18 antibody VK region #1.
                                                                                                      AAE27854 standard; protein; 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones T,
Baker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG67526 standard; protein; 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-FEB-2001; 2001EP-00103955.
05-APR-2001; 2001EP-00108291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2002; 2002WO-EP001690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones
                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.7
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr FJ,
Watkins J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-667054/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                 WO200266514-A2.
                                                                                                                                                                                       13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gillies S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanlon M,
                                                                                                                                                AAE27854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADG67526;
```

ô

Gaps

. 0

4; Indels

Length 113;

9

RESULT 7 ADG67526

셤 ઠે 임

ò

ŝ

```
WO200269232-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                    29-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                   Mus sp.
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel anti-human interleukin (IL)-18 rodent neutralizing monoclonal antibody having high affinity and useful for treating IL-18 mediated disorders such as multiple sclerosis, rheumatoid arthritis and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the light chain variable region of the mouse antibody 13G9. The antibody has high affinity for human interleukin-18 (IL-18) and is useful for treating and diagnosing IL-18-mediated disorders, e.g. autoimmune diseases such as multiple sclerosis, rheumatoid arthritis, type I or insulin dependent diabetes, inflammatory bowel disease and psoriasis. Specific changes can be introduced into the nucleotide sequences encoding the complementarity determining regions (CDRs) or framework regions of the variable light chain and heavy chain peptides. The resulting modified or fusion nucleic acid sequences can then be introduced into a plasmid for expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                  antibody 13G9; antiarthritic; immunosuppressive; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; fusion protein; immunological; major histocompatability complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                 antiinflammatory; antipsoriatic; interleukin-18; IL-18; autoimune disease; miltiple sclerosis; rheumatoid arthritis; type I diabetes; insulin dependent diabetes; IDBM; psoriasis; inflammatory bowel disease; complementarity determining region; CDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPYTFGGGTKLBIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.9%; Score 547; DB 3; Length 114; 92.0%; Pred. No. 1.7e-39; ive 4; Mismatches 5; Indels
                                                                  Mouse antibody 13G9 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Abdel-Meguid SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse 14.18 antibody VK modified epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE27842 standard; protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 3; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                            SMITHKLINE BEECHAM CORP SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor AH,
                                                                                                                                                                                                                                                                                                           17-MAR-2000; 2000WO-US007349
                                                                                                                                                                                                                                                                                                                                            99US-0125299P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 92.0
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-628249/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Holmes SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAA99642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 114 AA;
                                                                                                                                                                                                                                       WO200056771-A1.
                                                                                                                                                                                                                                                                                                                                            19-MAR-1999;
                                                                                                                                                                                                       Mus musculus
                                  25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-DEC-2002
                                                                                                                                                                                                                                                                         28-SEP-2000
AAB21363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                              (SMIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                Ho YS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
```

g ò 셤

8

XXXXXXXX

```
derived from a parent fusion protein, comprising first and second proteins/polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is ann-immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in combining known favourable properties of a composition or in creating new properties of a composition which alicits biological or pharmacological efficacy without having undesirable physiological effects such as nausea or gastric upset. The present sequence is mouse 14.18 antibody modified epitope. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DVVMTQSPGTLPVSLGERATISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGOSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New modified fusion protein with reduced immunogenicity, useful for combining favorable properties of a composition, comprises an immunoglobulin molecule linked to a non-immunoglobulin target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to an immunogenically modified fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGVPDRFSGSGSGTDFTLTISRLEAEDLAVYFCSQSTHVPPLTFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.4%; Score 532; DB 5; Length 113; 89.4%; Pred. No. 3.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamilton A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.18 antibody VK veneered modified epitope.
MHC; gastric upset; nausea; 14.18 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carter G,
Way JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 19; Page 77; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones T,
Baker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG67514 standard; protein; 113
                                                                                                                                                                                                                                                                                                                                                19-FEB-2001; 2001EP-00103955.
05-APR-2001; 2001EP-00108291.
                                                                                                                                                                                                                                                                              18-FEB-2002; 2002WO-EP001690
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gillies S, Carr FJ,
Hanlon M, Watkins J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-667054/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 113 AA;
                                                                                                                                       WO200266514-A2
```

Gaps

ဖ

92US-00827689. 92US-00889724. 92US-00894061.

93US-00009266 93US-00102852 94US-00286754

95US-00483389

```
DNA encoding mutant ICAM-R poly:peptide(s) - useful for diagnosis and treatment of cell adhesion based disease conditions e.g. inflammation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; Col 119-122; 111pp; English.
                                                                                                                                                                                                                                                                                                                   Vazeux R, Gallatin WM;
                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-530940/45.
                                                                                                                                                                                                                                                                                (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV54860
                                                                                                                                                                                     22-JAN-1993;
26-JAN-1993;
05-AUG-1993;
                                                                                                07-JUN-1995;
                          US5811517-A
                                                                                                                                                                                                                                              05-AUG-1994;
                                                            22-SEP-1998
                                                                                                                                    27-JAN-1992
                                                                                                                                                     26-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                asthma.
         The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (MHC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful to preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically non-poticity and having a retained biological molecule identified is useful for preparing a biological molecule with reduced immunogenicity in an having a retained desired biological activity, where the T-cell epitope is a lamer peptide. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                          Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide binding to MHC molecules.
                                                                                                                                                                                                                                                                                            Hamilton A;
                                                                                                                                                                                                                                                                                          Williams S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 21; Page 66; 85pp; English.
                                                                    2001EP-00106536.
2001EP-00106538.
2001EP-00106899.
                                                                                                                                                                                                                                                                                          Jones T,
18-FEB-2002; 2002WO-EP001688
                                                                                                                             2001EP-00107012
                                                                                                                                              2001EP-00107568
                                                                                                                                                             2001EP-00110220
                                                                                                                                                                                  2001EP-00113228
                                                                                                                                                                                                 2001EP-00124965
                                                                                                                                                                                                                12-NOV-2001; 2001EP-00126859
                                                                                                                                                                                                                                                    (MERE ) MERCK PATENT GMBH
                                                                                                                                                                                                                                                                                          Carter G,
                                                                                                                                                                                                                                                                                                                          WPI; 2002-750424/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 113 AA;
                                                                                                                     20-MAR-2001;
27-MAR-2001;
25-APR-2001;
                                                                                     15-MAR-2001;
20-MAR-2001;
                                                                                                                                                                                                 19-OCT-2001;
                                                                    15-MAR-2001;
                                                   08-MAR-2001;
                                                                                                                                                                              30-MAY-2001;
                                                                                                                                                                                                                                                                                        Carr FJ,
```

```
20-NOV-1998 (first entry)
                                                                        Conservative
                         Query Match
Tonal Similarity
        Sequence 116 AA;
                                                                   Matches 100;
                                                                                                                                                                                                                                                                                                             AAW76126;
                                                                                                                                                                    61
                                                                                                                                 a
                                                                                                                                                                                                셤
                                                                                                      ò
                                                                                                                                                                  ò
                                      0
                                                                      9
                                                                                                  9
                                                              1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Human; ICAM-R; intercellular adhesion molecule; adhesion; treatment;
inflammatory condition; asthma; tumour growth; metastasis;
viral infection; antibody ICR-8.1.
                                                                                                                            SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                Humanised murine antibody ICR-8.1 light chain amino acid sequence.
                                    ö
89.4%; Score 532; DB 5; Length 113; 89.4%; Pred. No. 3.3e-38; Live 6; Mismatches 6; Indels
                                                                                                                                                                                                                                         AAW71256 standard; protein; 116 AA
                                                                                                                                                                                                                                                                                                                         (first entry)
                                 Conservative
                                                                                                                                                                                                                                                                                                          (revised)
Query Match
Best Local Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                                                                     25-MAR-2003
18-NOV-1998
                                                                                                                             61
                                                                                                                                                                                                                                                                       AAW71256;
```

61

셤 8

8

RESULT 11

Mus sp. Homo sapiens

Synthetic.

```
The present sequence represents the humanised light chain of murine antibody ICR-81. This antibody is specific for ICAM-R (intercellular adhesion molecule-R). ICAMS are polypeptides that are expressed on blood vessel endothelial cell surfaces and are involved in the adhesion sevents in various conditions. ICAM-R variants (see AAW71264-69) can be used to nonspecific immune responses, asthma, tumour growth and/or metastasis and viral infections. The ICAM variants are produced recombinantly, from expression libraries of mutated sequences, and the ones that are claimed are the ones that have been found to be especially involved in adhesion events. They can also be used to raise antibodies, also for use as the appearance or diagnostic agents. (Updated on 25-MAR-2003 to correct PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Intercellular adhesion molecule; human; ICAM-R; modulator; 14.3.3 family; HS1-beta; tubulin; inhibitor; stimulator; effector; immune response; inflammation; disorder; T cell activation; macrophage; Crohn's disease; adult respiratory distress syndrome; stroke; multiple sclerosis; asthma; rheumatoid arthritis; tumour growth; human immune deficiency virus; infection; diabetes; graft vs. host disease; passive immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 DIVMIQSPLSLPVIPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIXKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.2%; Score 530.5; DB 2; Length 116;
88.5%; Pred. No. 4.5e-38;
ive 9; Mismatches 3; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ICR-8.1 V-K region PCR product protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW76126 standard; protein; 116 AA
```

```
The invention relates to humanised ICR-1.1 and ICR-8.1 antibodies targeted to the human intercellular adhesion molecule polypeptide (ICAM-R) polypeptide. Antibodies specific for ICAM's are potentially useful as therapeutic compounds, for treating e.g. immune-mediated inflammatory conditions (e.g. graft-versus-host disease), asthma, tumours or viral infections. Monoclonal antibodies specific for ICAM-R, or their conjugates formed with e.g. toxins or radionuclides are useful for therapeutically targeting or detecting neovascularisation sites. The present sequence represents the amino acid sequence of the VK region of the humanised antibody ICR-8.1
monoclonal antibody; therapeutic; inflammatory; asthma; tumour; sus-host disease; viral infection; toxin; radionuclide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised antibodies specific for intercellular adhesion molecule polypeptide - useful for therapeutic or diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICAM-R, murine; intercellular adhesion molecule; phosphorylation; protein kinase C; modulator; ICR-8.1; VH region; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.2%; Score 530.5; DB 2; Length 116; 88.5%; Pred. No. 4.5e-38; ive 9; Mismatches 3; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised murine antibody ICR-8.1 VK region HuVK protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 13; Col 131-132; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY50753 standard; protein; 116 AA
                                                                                                                                                                                                                                                                                        92US-0089724.
92US-00894061.
93US-00009266.
93WO-US000787.
93US-00102852.
                                                                                                                                                                                                                                95US-00487113
                                                                                                                                                                                                                                                                       92US-00827689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 100; Conservative
                                         neovascularisation site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vazeux R, Gallatin WM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-023535/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV69174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
Homo sapiens.
                                                                                    Mus sp.
Homo sapiens.
                                                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-FEB-2000
                                                                                                                                             US5837822-A.
                                                                                                                                                                                      17-NOV-1998
                                                                                                                                                                                                                                                                                           26-MAY-1992
05-JUN-1992
                                                                                                                                                                                                                                                                                                                                    22-JAN-1993
26-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY50753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
  ICR-8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
AAY50753
  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a human ICR-8.1 V-K region amplified PCR product. This sequence is used in the isolation of a novel human intercellular adhesion molecule, ICAM. This sequence is used in a method which investigates modulators of the interaction between ICAM-R and the 14.3.3 family member HSI-beta and tubulin. An anti-ICAM-R peptide, can block, inhibit or stimulate ligand/receptor interactions involving ICAM-R, particularly its effector functions involved in involving ICAM-R, particularly its effector functions involved in treat or monitor inflammation, disorders involving T cell activation or macrophages, e.g. adult respiratory distress syndrome, stroke, Crohn's disease, multiple sclerosis, rheumatoid arthritis, asthma, tumour growth, human immune deficiency virus infection, diabetes, graft vs. host disease and many others. Antibodies may also be used for passive immunisation, for purifying idetecting or quantifying ICAM-R and for identifying ICAM-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying compounds that modulate interaction of intracellular adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Intercellular adhesion molecule polypeptide; ICAM-R; humanised; ICR-1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecule R - with ligands HS1-beta and tubulin using two-hybrid assay, useful for treating inflammation, T cell activation etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 DIVWIQSPLSLPVIPGEPASISCRSSQSLVHSNGDIYLHWYLQXPGQSPQLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYXCSQSTHV-PYTFGQGTKVEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.2%; Score 530.5; DB 2; Length 116; 88.5%; Pred. No. 4.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised antibody ICR-8.1 Vk region (HuVK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; Col 120-121; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW81450 standard; protein; 116 AA.
                                                                                                                                                                                  92US-00827689.
92US-00889724.
92US-000894061.
93US-00009266.
93US-00102852.
94US-00286754.
                                                                                                                                             95US-00482882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 88.5
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Gallatin WM, Vazeux R;
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-386989/33.
                                                                                                                                                                                                                                                                                                                                                          CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV56402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 116 AA;
                                                                                                                                                                                                                                                                                                                                                          SODI (-SODI)
                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-1999
                                                                                                                                             07-JUN-1995;
                                                                                                                                                                                                                                                                                                                05-AUG-1994;
                                                            US5773218-A
                                                                                                    30-JUN-1998
                                                                                                                                                                                                          26-MAY-1992
05-JUN-1992
                                                                                                                                                                                                                                                   22-JAN-1993
                                                                                                                                                                                                                                                                       26-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW81450
```

6 64

ઠે 셤 ઠે g

Gaps

1;

Φ

Synthetic.

```
This invention describes a novel method for identifying a compound that modulates phosphorylation of human intercellular adhesion molecule polypeptide (IGAM-R) by protein kinase C isoform. The method comprises:

(a) exposing a purified peptide consisting of the cytoplasmic domain of ICAM-R to protein kinase C isoform and labeled adenosine triphosphate in the presence and absence of a test compound; (b) measuring labeled that affects transfer of the peptide; and (c) identifying a test compound that affects transfer of the labeled phosphate as a modulator compound. The method is useful for identifying compounds that modulate the phosphorylation of human intercellular adhesion molecule polypeptide which might form the basis for the development of therapeutic and diagnostic agents. This sequence represents the humanised mutine antibody ICR-8.1 VK region (HuVK) which is used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                       Identifying modulators of protein kinase C phosphorylation of human intercellular adhesion molecule polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                    Example 14; Col 137-138; 122pp; English.
                                                                                                                                              92US-00889724.
92US-00894061.
93US-00009266.
93WO-US000787.
93US-00102852.
                                                                                                  96US-00720420
                                                                                                                                92US-00827689
                                                                                                                                                                                                                                                                                          Vazeux R;
                                                                                                                                                                                                                                                                                                                         2000-022778/02.
                                                                                                                                                                                                                                                              CORP.
                                                                                                                                                                                                                                                                                                                         WPI; 2000-022778/
N-PSDB; AAZ24316.
                                                                                                                                                                                                                                                          (ICOS-) ICOS
                                                                                                                                                                                                                                                                                         Gallatin WM,
                                                                                                27-SEP-1996;
                                                                                                                                              26-MAY-1992;
05-JUN-1992;
22-JAN-1993;
                                US5989843-A.
                                                                23-NOV-1999
                                                                                                                                                                                                           05-AUG-1993
                                                                                                                               27-JAN-1992
                                                                                                                                                                                             26-JAN-1993
   Mus sp.
```

1; 89.2%; Score 530.5; DB 3; Length 116; 88.5%; Pred. No. 4.5e-38; Indels 1. Conservative Local Similarity Les 100; Conserv Sequence 116 AA; Query Match Best Loca Matches

9 64 1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF ß

요

ò

셤

```
AAB13046 standard; protein; 116 AA
                       19-DEC-2000 (first entry)
                AAB13046;
RESULT 15
```

Protein sequence of humanised ICR-8.1 Vk.

Anti-human immunodeficiency virus; HIV; cytostatic; ICAM-R; ARDS; stroke; intercellular adhesion molecule; immunoglobulin heavy chain; septicaemia; inflammatory conditions, glomerulonephritis; arthritis; dermatosis; haemodialysis; leukapheresis; ulcerative colitis; Crohn's disease; necrotising enterocolitis; atherosclerosis; psoriasis, asthma; transplant rejection; diabetes; tumour.

```
This invention relates to a hybrid fusion protein comprising an intercellular adhesion molecule (ICAM-R) amino acid fragment at its amino conternius and a constant domain of an immunoglobulin heavy chain at its carboxy terminus. ICAM-R polypeptides are useful for treating and monitoring inflammatory conditions such as adult respiratory distress correction, multiple organ injury syndrome secondary to septicaemia or trauma, reperfusion injury of tissue, acute glomerulonephritis, reactive curvative colitis, crohm's disease, necrotising archarotesis, ulcerative colitis, Crohm's disease, necrotising cherosolatis, granulocyte transfusion associated syndrome, atherosclerosis and cytokine induced toxicity. ICAM-R polypeptides are also useful for treating conditions resulting from a response of the specific immune system in a mammal e.g. psoriasis, organifismus contribries, diabetes and autoimmune diseases including Raymand's cransplant rejection and autoimmune diseases including Raymand's cransplant rejection and autoimmune diseases including Raymand's cransplant rejection and autoimmune given manual e.g. psoriasis, organifismus cransplant rejection and autoimmune diseases including Raymand's cransplant rejection and autoimmune diseases including Raymand's cransplant rejection and autoimmune diseases including Raymand's cransplant rejection and succidents, multiple sclerosis, rheumatoid carthritis, diabetes and lupus erythematosus. ICAM-R polycesent ICAM-R DNA fragments used in the production of ABAB1305 represent ICAM-R DNA and protein sequences. Sequences AAA97115-A97128, AAA971121, AAA971124, AAA971124, AAA971124, AAA971124, AAA971124, AAA971124, AAA971124, AAA971124, AAA971125, AAAA971132, AAA971134, AAA97114 represent primers used in the production of humanised anti-ICAM-R antibody ICR-11, and fragments of the humanised anti-ICAM-R antibody ICR-11, and fragments of the humanised anti-ICAM-R antibody and honey represent primers used in the seminance used in the seminance used anti-ICAM-R antibody ICR-11, and fragme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hybrid fusion proteins comprising intercellular adhesion molecule or its variants useful, for treating inflammatory conditions, Crohn's disease, atherosclerosis and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ICR-1.1 sequences. DNA and peptide sequences used in the production of the chimeric protein of the invention include AAA97177-A97188 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 13; Col 121-122; 109pp;
                                                                                                                                                                                                     92US-00827689.
92US-00889724.
92US-00894061.
93US-0009266.
                                                                                                                                                                                                                                                                                            93WO-US000787.
93US-00102852.
94US-00286754.
                                                                                                                                                             95US-00475680
                                                                                                                                                                                                                                                                                                                                                                                                                                Vazeux R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-542449/49.
                                                                                                                                                                                                                                                                                                                                                                                    (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAA97144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hybrid fusion
                                                                                                                                                                                                                                                                                                                                                                                                                            Gallatin WM,
                                                                                                                                                         07-JUN-1995;
                                                                 US6100383-A.
                                                                                                                                                                                                                                                                                                                                         05-AUG-1994;
                                                                                                              08-AUG-2000
                                                                                                                                                                                                        27-JAN-1992
                                                                                                                                                                                                                                                                                            26-JAN-1993
05-AUG-1993
                                                                                                                                                                                                                             26-MAY-1992
                                                                                                                                                                                                                                                                       22-JAN-1993
```

5 DIVWTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF

g δ

ò

1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF Gaps 1; Indels 89.2%; Score 530.5; DB 3; llarity 88.5%; Pred. No. 4.5e-38; Conservative 9; Mismatches 3; Query Match Best Local Similarity Matches 100; Conserv

Length 116;

09 64

61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113

65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSOSTHV-PYTFGQGTKVEIK 116

Search completed: April 18, 2005, 10:00:56 Job time : 65 secs

This Page Blank (uspto)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

April 18, 2005, 09:57:11; Search time 11.5 Seconds (without alignments) 945.434 Million cell updates/sec Run on:

US-10-737-208A-1 595 1 DVVMTQTPLSLPVTPGEPAS......SQSTHVPPLTFGAGTKLELK 113 score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMWAKIES Description	In light chain V	kappa		kappa chain	kappa	kappa chain	ibody Fab Je	kappa	kappa chain	i-DNA autoan	kappa	Ig kappa chain V	kappa	kappa chain	kappa chain	Ig kappa chain V	Ig kappa chain V	Ig kappa chain pre	kappa chain	anti-digoxin trans	b	b	b	kappa chain			Ig light chain V	kappa	
ID OI	B41940	G34903	PT0178	838715	B30577	E27887	853750	PT0359	B34904	PL0205	PL0257	B27887	B32513	C34904	832189	A27887	D27887	D34904	KVMS26	PH0106	D32530	B31485	C27887	9009	244	D29380	838719	971	026300
DB	10	~	~	~	7	7	~	7	7	~	7	7	~	7	7	7	~	~	, -1	~	7	7	7	7	7	~	7	7	^
Length	113	131	131	115	131	112	112	118	131	113	111	112	131	131	112	112	112	131	113	132	107	112	112	115	131	131	112	112	130
% Query Match	90.8	90.0	90.0	89.3	89.2	89.0	88.8	88.8	88.8	88.7	88.3	88.3	88.2	88.2	88.0	87.8	87.6	87.5	87.1	87.1	87.0	87.0	86.8	86.5	96.0	86.0	85.1	85.1	84.7
Score	540.5	'n	535.5	_;	0	Ψ.	m	m	m	_	ıΩ	:0	T #	**	~	\sim	-	\circ	m	œ	7	7	516.5	4	щ		506.5	S	504
Regult No.	-	8	9	4	S	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

anti-DNA autoantib	Ig kappa chain - m		Ig kappa chain v r			light	kappa	kappa	kappa		light	kappa	kappa	light	kappa
L0203	028	376	112	172	203	131	30	07	87	35	30	67	65	34	67
PL(852	B39;	S16	8427	PC4	PH10	E325	A318	F27887	8263	PH10	A329	8388	PH1034	B32967
2 PL(2 852	2 B392	2 \$16	2 8427	2 PC4;	2 PH10	2 E325	2 A318	2 F278		2 PH10		2 \$388	2 PH10	2 B329
7	7	~	219 2 816	~	7	~	~	~	0	7	~	~	~	7	
113 2	219 2	131 2	~	217. 2	219 2	103 2	108 2	112 2	112 2	110 2	103 2	114 2	219 2	103 2	114 2
84.3 113 2	84.3 219 2	84.1 131 2	219 2	83.8 217 2	83.8 219 2	83.4 103 2	83.3 108 2	83.3 112 2	82.9 112 2	82.8 110 2	103 2	82.1 114 2	82.1 219 2	103 2	114 2

ALIGNMENTS

```
Ig light chain V region G2b, autoantibody BV04-01 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: O4-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Ju1-2004
C;Accession: B41940; PL0206
R;Herron, J.N.; He, X.M.; Ballard, D.W.; Blier, P.R.; Pace, P.E.; Bothwell, A.L.; Voss L.Proteins 11, 159-175, 1991
A;Title: An autoantibody to single-stranded DNA: comparison of the three-dimensional stranscentible autoantibody wull:92086633; PMID:1749770
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary, not compared with conceptual translation
A;Status: preliminary, not compared with conceptual translation
A;Status: preliminary, not compared with conceptual translation
A;Residues: 1-113 <HBKP.
A;Cross-references: UNIPROT:Q8VCI6
A;Cross-references: UNIPROT:Q8VCI6
A;Note: sequence extracted from NCBI backbone (NCBIP:70714)
B;Smith, R. G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from PA;Reference number: PL0198; MUID:90309768; PMID:2114528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: immunoglobulin F:16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:24-39/Region: complementarity-determining 1
F:55-61/Region: complementarity-determining 2
F:94-102/Region: complementarity-determining 3
F:101-113/Region: JH region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-113 <SMI>
```

Gaps 1; Length 113; 90.8%; Score 540.5; DB 2; Length 1 93.8%; Pred. No. 6.1e-43; tive 3; Mismatches 3; Indels Matches 106; Conservative Query Match Best Local Similarity

ï 9

1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 셤 ð ò

RESULT 2 G34903

셤

```
F;19-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                  g
                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig Kappa chain precursor V region (IdBS.7) - mouse (fragment)

G.Species: Mus musculus (house mouse)

G.Species: Mus musculus (house mouse)

G.Accession: PT018

F. Ferfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.

Mol. Immunol. 28, 505-515, 1991

A.Fitle: Specificity and variable region cDNA sequence of an isogeneic monoclonal antiid

A.Feference number: PT0174; MUID: 91287738; PMID: 1712074

A.Reseion: PT078

A.Resion: PT078

A.Resion: PT078

A.Resion: PT078

A.Resion: T131 < PER.

A.Resion: T131 < PER.

A.Resion: T131 < PER.

A.Resion: T131 < PER.

A.Cross-references: UNIPROT: Q8VCI6

A.Resion: T131 < PER.

A.Cross-references: UNIPROT: Q8VCI6

A.Resion: T131 < PER.

A.Cross-references: Train BALB/C

G.Superfamily: immunoglobulin v region; immunoglobulin homology

C.Keywords: heterotetramer; immunoglobulin homology < IMM>
fittle: Active site structure and antigen binding properties of idiotypically cross-real Reference number: A34903; MUID:90094387; PMID:2104617
                                                                                                                                                            A;Cross-references: GB:M12181; GB:U05237; GB:U05238; NID:g639654; PIDN:AAA61588.1; PID::
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                 DVVMTQTPLSLPVSLGBQASISCRSSQSLIHSNGNTYFHWYLQKPGQSPKLLIYKVSNRF 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: S38713
A;Accession: S38715
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <CIM>A;Cross-references: EMBL:X76015; NID:9416094; PIDN:CAA53602.1; PID:91334077
C;Reywords: heterotetramer; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38715
R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
                                                                                                                                                                                                                                                                                                                                                                     1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHINGNTYLHWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK
                                                                                                                                                                                                                                                                                    Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 131;
                                                                                               A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-131 <BED>
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
.
                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                               Score 535.5; DB Pred. No. 2e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 535.5; DB
Pred. No. 2e-42;
4; Mismatches
                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                               90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.0%;
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                    Matches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
S38715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                             요
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
```

```
Rikoffler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theof. Sxp. Med. 161, 805-815, 1985
J. Exp. Med. 161, 805-815, 1985
J. Fritle: Genetic elements used for a murine lupus anti-DNA autoantibody are closely relamble A; Reference number: A30577; WUID:85159423; PMID:3920343
A; Accession: B30577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-112 <CAT>
A;Experimental source: strain Balb/c
A;Experimental source: strain Balb/c
A;Experimental source: strain Balb/c
C;Comment: This sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Structural and functional implications of a restricted antibody response to a d. A;Reference number: A91043; MUID:86300658; PMID:2427335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                9
                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain precursor V region (MRL10) - mouse (fragment)
C;Species: Was musculus (house mouse)
C;Date: 04-May-1989 #sequence_revision 04-May-1989 #text_change 09-Jul-2004
C;Accession: B30577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region (H146-24B3) - mouse
C;Species: Mus musculus (house mouse)
C;Daces 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C;Accession: E27887
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
                                                                                                                                         20 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF
                                                                                                          1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DWWTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPK1LIHKVSNRF
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                               SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
;
        Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-131 <KOF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q8VCI6
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: hereroterramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.0%; Score 529.5; DB 2; llarity 91.2%; Pred. No. 6.2e-42; Conservative 4; Mismatches 5;
     Score 531.5; DB 2
Pred. No. 4.2e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.2%; Score 530.5; DB 2 ilarity 91.2%; Pred. No. 5.9e-42; Conservative 4; Mismatches 5
                                                        6; Mismatches
Query Match
Best Local Similarity 90.3%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
```

```
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity
                                                                                                                                                                  A; Accession: B34904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ~
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                   artibody Fab Jel 103 light chain - mouse C.Species: Mus musculus (house mouse) C.Species: Mus musculus (house mouse) C.Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 C.Accession: 853750 C.Accession: 853750 C.Accession: Bouthillier, F.; Li, Y.; Kuderova, A.; Lee, J.; Cygler, M. J. Mol. Biol. 243, 283-297, 1994 A.Title: Preparation, characterization and crystallization of an antibody Fab fragment A.Reference number: 853750; MUID:95018269; PMID:7523684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004 C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004 C.Accession: PT0359
R.Shefner, R.; Kleiner, G.; Turken, A.; Papazian, L.; Diamond, B.
J. Exp. Med. 173, 287-296, 1991
A;itle: A novel class of anti-DNA antibodies identified in BALB/c mice. A;Reference number: PT0352; MUID:91108325; PMID:1988536
A;Accession: PT0359
A;Molecule type: mRNA
A;Residues: 1-118 <SHE>
A;Coss references: UNIPROT:08VCI6
A;Experimental source: strain BALB/c
C;Comment: This protein is an anti-double-stranded DNA antibody.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;19-98/Domain: immunoglobulin homology <IMM>
DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g kappa chain V region (R4A.12) - mouse (fragment)
.Species: Mus musculus (house mouse)
.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
.Accession: PT0359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                      SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHV-PYTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHV-PRTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHV-PWTFGGGTKLEIK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSOSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-112 <POK>
A;Cross-references: UNIPROT:Q8VCI6
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9 B34904 Ig kappa chain precursor V region (12-40 and 5-14) - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.8%; Score 528.5; DB 2;
91.2%; Pred. No. 7.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 88.8%; Score 528.5; DB 2 Best Local Similarity 91.2%; Pred. No. 8.1e-42; Matches 103; Conservative 4; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 91.2
Matches 103; Conservative
                                             61
                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
g
                                                                                       g
                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            유
```

```
A;Residues: 1-131 <BED>
A;Residues: 1-131 <BED>
A;Cross-references: GB:M32384; GB:J05237; GB:J05238; NID:g639656; PIDN:AAA61589.1; PID:c
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: PL0205
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from }
A;Reference number: PL0198; MUID:90309768; PMID:2114528
A;Accession: PL0205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C'Species: Mus musculus (house mouse)
C'Species: Mus musculus (house mouse)
C)Date: 1.6-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: PLO257
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J. R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J. A;Tile: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PLO231; MUID:90111618; PMID:2104919
                                                                                                                                                                                            cross-re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ï
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #text_change 21-Jul-2000
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C;Accession: B34904; H34903
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Baol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically A;Reference number: A34903; MUID:90094387; PMID:2104617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-DNA autoantibody BV16-19, kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-113 <SMI.>
A; Residues: 1-113 <SMI.>
A; Cross-references: GB:X53645; NID:g50194; PIDN:CAA37696.1; PID:g930140
C; Superfamily: immunoglobulin 'V region; immunoglobulin homology
F; 16-95/Domain: immunoglobulin homology <IMM>
F; 16-95/Domain: complementarity-determining 1
F; 55-61/Region: complementarity-determining 2
F; 94-102/Region: complementarity-determining 3
F; 101-113/Region: JH region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVPDRFSGSGSGTDFTLKISRVGAEDLGVYFCSQSTHV-PLTLGAGTKLELK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHV-PWTFGGGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 113;
                                                                                                                                                                                                                                                                                                   A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain V region (anti-DNA, DPIVK) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.8%; Score 528.5; DB 2;
llarity 91.2%; Pred. No. 9e-42;
Conservative 4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.7%; Score 527.5; DB 2 92.0%; Pred. No. 9.5e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
```

us-10-737-208a-1.rpr

```
A; Molecule type: mRNA

A; Residues: 1-131 < ABD. A

A; A; Cross-references: UNIPROT: Q8VCI6

B; Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.

B; Baol. Chem. 264, 1565-1569, 1989

A; Title: Comparison of variable region primary structures within an anti-fluorescein idi

A; Reference number: A31485; MUID: 89109167; PMID: 2492278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 DVVMTQTPLSLPVSLGDQASFSCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain precursor V region (3-24) - mouse
Cispecies: Whus musculus (house mouse)
Cibate: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
Cibates: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
Cibacesion: C34604; I31485
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, I33-139, 1990
A;Title: Active site structure and antigen binding properties of idiotypical
A;Reference number: A34903; MUID:90094387; PMID:2104617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32189
                                                                                                                                                                                                                                                                                                                                                                                1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
A,Molecule type: DNA A,Residues: 1-131 <KOF>
A,Residues: 1-131 <KOF>
A,Cross-references: GB:M20828; NID:g196937; PIDN:AAA38843.1; PID:g196938
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHV-PYTFGSGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHV-PWTFGGGTKLEIK 131
                                                                                                                                                                                                                           Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: protein
A;Residues: 20-52 <BE2.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
;
                                                                                                                                                                                                                     88.2%; Score 524.5; DB 2; 90.3%; Pred. No. 2.1e-41; ive 5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.2%; Score 524.5; DB 2 90.3%; Pred. No. 2.1e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Izui, S.
submitted to the EMBL Data Library, February 1993
submitted number: 832185
A;Accession: 832189
A;Accession: 932189
A;Scatus: preliminary
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                              Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: C34904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: I31485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       832189
                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cidence: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
Cidecesion: B27887
Cidencesion: B27887
Cidencesion: B27887
EMBO J. S. 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a dividence number: A91043; MUID:86300658; PMID:2427335
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Residues: 1-112 cdpr
A;Comment: This sequence was determined from the germline gene
C;Comment: This sequence was isolated from a hybridoma protein that binds influenza virus PC;Superfamily: immunoglobulin V region; immunoglobulin
C;Superfamily: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain precursor V region (MRL4) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 2-1-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: B32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; J.Clin. Invest. 82, 822-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and A;Reference number: A94689; WUID:88331394; PMID:3138286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g kappa chain V region (H37-62) - mouse
Species: Mus musculus (house mouse)
Jabte: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
Accession: B27887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SGVPDRFSGSGSGTDFTLKISRVEADDLGVYFCSQSTHIPD-TFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLEL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 112;
                                                                         Across references .UNIPROT:08VCI6
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-95/Domain: immunoglobulin homology <IMM>
F;24-39/Region: complementarity-determining 1
F;55-61/Region: complementarity-determining 2
F;55-61/Region: framework 2
F;55-61/Region: framework 3
F;94-102/Region: framework 3
F;91-111/Region: framework 4
F;03-111/Region: framework 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 525.5; DB 2;
Pred. No. 1.4e-41;
5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.3%; Score 525.5; DB 2; Best Local Similarity 89.4%; Pred. No. 1.4e-41; Matches 101; Conservative 6; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 91.1
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
B32513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

idiotypically cross-rea

Gaps

1;

9

Gaps

ï

```
A;Cross-references: EMBL:X70094; NID:g288255; PIDN:CAA49699.1; PID:g288256 (S.Ugerfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroteramer; immunoglobulin homology < IMM> P:16-95/Domain: immunoglobulin homology < IMM>
```

									_
Query Match	ch 1 similarity	88.0%;	Query Match 88.0%; Score 523.5; DB 2; Length 112;	; ;	Length 113				
Matches 1	102; Conserva	ative	Matches 102; Conservative 4; Mismatches 6; Indels 1; Gaps	. ; 9	Indels	1,	Gaps	1,	
	1 DVVMTQTPLS	LPVTPGEPA	1 DVVMIQIPLSLPVIPGEPASISCRSSQSLVHRNGNIYLHWYLQKPGQSPKLLIHKVSNRF 60	YLHWY	TOKPGOSPKI	LLIHK	VSNRF 6		
	1 DVVMTXTPLS	LPVSLGDQA	DVVMTXTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 60	LE HWY	TQKPGQSPKI	TĂ.	VSNRF 6	6	

ò 셤 8 g Search completed: April 18, 2005, 10:06:46 Job time : 11.5 secs

This Page Blank (uspto)

```
mus musculu
mus musculu
mus sp. b3(
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                          homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homo sapien
mus musculu
mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homo sapien
homo sapien
mus musculu
mus musculu
                                                    April 18, 2005, 09:42:15; Search time 84.5 Seconds (without alignments) 684.792 Million cell updates/sec
                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                        US-10-737-208A-1
595
1 DVVMTQTPLSLPVTPGEPAS......SQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                        Q6552C
Q65447
Q65418
Q6418
Q684Cd
Q684Cd
Q684Cd
Q6810
Q6810
P01615
P01615
P01615
P01615
P01628
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                        1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                       Q652C0
Q652Q7
Q6P1H6
Q9UL80
KV2D HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KV2E HUMAN
KV2F HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KV4A_HUMAN
Q65ZI1
KV3B_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KV2C_MOUSE
KV2A_MOUSE
KV1_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
HUMAN
MOUSE
MOUSE
                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                               KV2G MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
HUMAN
MOUSE
MOUSE
MOUSE
HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KV2A_HUMAN
                                   OM protein - protein search, using sw model
                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OBNEKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KV2B
                                                                                                                                                                                                                                                          UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                     Query
Match Length DB
                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                            Seguence:
                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                           Database
                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                     Result
                                                                                                                                                                                                                                                                                                                                                               No.
```

Q723y5 homo sapien P01660 mus musculu Q6pile homo sapien P01663 mus musculu Q91178 homo sapien P01672 mus musculu P01672 mus musculu Q92099 mus musculu P01670 mus musculu	د د	nence update) lotation update) 10. Craniata; Vertebrata; Euteleostomi; Sciuroqnathi; Muridae; Musinae; Mus.	chain variable region from a mouse	J83). in was isolated from an IgG2a hybridoma it. it. 1. Hybridoma; Immunoglobulin V region;	Framework-1. Complementarity-determining-1. Framework-2. Complementarity-determining-2. Framework-3. Complementarity-determining-3. Framework-4. By similarity. F9F39CE949A84C2A CRC64;
2 C7Z3YS C6FIL8 2 C6FIL8 2 C6FIL8 1 KV3K MOUSE 2 C9UL7 8 KV3T MOUSE 1 KV3T MOUSE 1 KV3T MOUSE 2 C920E9 1 KV3D HUMAN 1 KV3P MOUSE 1 KV3P MOUSE 2 C6GMV9 1 KV3L MOUSE 2 C6GMV9	ALIGNMENTS PRT; 113 AA	(6 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	404298; 		Σ. ;
\$8.7 86 \$58.7 111 \$58.7 236 \$58.2 1111 \$58.0 1109 \$57.6 1111 \$57.6 1109 \$57.5 1110 \$57.5 1110 \$57.5 1110	STANDARD;	(Rel. 01, (Rel. 01, (Rel. 44, in V-II re (Mouse). etazoa; Ch	# # D D I	BIOGNEMISETY ZZ:1153-1158 (1983)!- MISCELLANEOUS: This chain was protein that binds digoxin. PIR; A01914; KW826. PIRSP; Q99M37; 1191. InterPro; IPR007110; Ig-like. InterPro; IPR001596; Ig_v. Pfam; PF00047; ig; 1. PRMST; SM00406; IGv; 1. PRMST; SM00406; IGv; 1. PROSITE; PS50815; IG_LIKE; 1. Direct protein sequencing; Hybrid	antibody. 1 23 24 39 24 54 55 61 62 93 94 102 112 23 113 113 113 AA; 12273 MW;
332 332 332 344 35 35 36 36 36 37 36 37 36 37 37 37 37 37 37 37 37 37 37 37 37 37	RESULT 1 KV2G MOUSE ID KV2G MOUSE	P01631; 21-JUL-1986 (Rel. 01 21-JUL-1986 (Rel. 40 05-JUL-2004 (Rel. 44 Ig kappa chain V-II Mus musculus (Mouse) Bukaryota; Metazoa; Mammalia; Eutheria;	NCBI_TaxiD=10090; [1] SEQUENCE. STRAIN=A/J; MEDLINE=83178921; Novocny J., Margo "Amino acid seque anti-digoxin hybr.	blochemistry Zilliss -!- MISCELLANBOUS: II protein that bin protein that bin RSP; Q99M37; III9. III terPro; IPR001110; InterPro; IPR001110; InterPro; IPR00110; RAMAT; SMO406; IGV; BRART; SMO406; IGV; Direct protein seque	Monoclonal a DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DISULFID NON TER
	RESI KV2(0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	R R R R R R R R R R R R R R R R R R R	**************************************	XX TITE TITE SO

1; 60 60

1; Gaps

Query Match 87.1%; Score 518.5; DB 1; Length 113; Best Local Similarity 88.5%; Pred. No. 2.4e-46; Matches 100; Conservative 7; Mismatches 5; Indels 1

셤

ઠે

a

ò

```
Pfam; PF07654; C1-set;
SMART; SM00409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissum=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              обрін6
Обрін6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
106PIH6
10 AC 06PIH6
10 TO 5-JU
10 TO 05-JU
11 TO 05-JU
1
유보유유유유 유구
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

C STRAIN=Balb/c; TISSUE=Spleen;

MEDINE=56319565; bubMed=8768802;

MEDINE=56319565; bubMed=8768802;

MA Kipp B., Schlaak M., Becker W.M.;

"Cloning and expression of a recombinant mouse Fab-fragment recognizing a defined linear epitope of Chironomus thummi major

T allergen Chi t I.";

T allergen Chi t I.";

T allergen Chi t I.";

MEDINE=563199; CAR85724.1;

MEDINE: 27499; CAR85724.1;

MEDINE: 1PR003599; Ig.

InterPro; IPR003599; Ig.

InterPro; IPR003599; Ig.

InterPro; IPR003596; Ig.

MHC.

MEDINE: 27499; CI-set;

MEDINE: 27499; MHC.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPG-TFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-292020094. PubMed=1924323;
MEDLINE-292020094. PubMed=1924323;
MEDLINE-292020094. PubMed=1924323;
"B3 (FV) - PE338KDEL, a single-chain immunotoxin that causes complete regression of a human carcinoma in mice.";
Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp.

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;
                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Kappa light chain C region (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.1%; Score 494.5; DB 2;
85.8%; Pred. No. 1.7e-43;
1ve 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWART; SM00409; IG; 2.
SWART; SM00409; IG; 1.
PRAST; SM00406; IGC1; 1.
PROSITE; PS00835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNROWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q652Q7
Q652Q7
Q652Q7
25-OCT-2004 (TrEMBLrel. 28, C
25-OCT-2004 (TrEMBLrel. 28, L, L
25-OCT-2004 (TrEMBLrel. 28, L, B3 (FV)-PE40 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 85.8
Matches 97; Conservative
                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                    RESULT 2
Q652C0
                                                                                                                                      ACCOCCOS DIT STATE STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MILAGUSER R.D., Feingold B.A., Grouse L.H., Derge J.G.,

MILAGUSER R.D., Colling F.S., Magner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.L., Mang J., Hashe F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Parage C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHV-PFTFGSGTKLEIK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                        1,
                                                                                                                                                                                                                                                                                                                                                 82.6%; Score 491.5; DB 2; Length 248; 83.2%; Pred. No. 4e-43; ive 10; Mismatches 8; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BCO134142; AAH34142.1; -.
HASSP; PO1837; IRBS.
InterPro; IPR0013599; Ig.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003506; Ig.MHC.
InterPro; IPR003567; Ig.MHC.
Pfam: PF07654; CI-set; I.
                                                                                                                                                                                                                                                                                7A3759B43E570950 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
InterPro; IPR003599; IG.
InterPro; IPR00310; IG-like.
InterPro; IPR00310; IG-like.
Pfam; PF00047; ig; 2.
SWART; SW00409; IG; 2.
PROSITE; PS50839; IG LIKE; 2.
PROSITE; PS50839; IG LIKE; 2.
                                                                                                                                                                                                                                                                                    26634 MW;
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.2%,
Local 94; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                         SEQUENCE 248 AA;
```

```
21-JUL-1986 (Rel. 01, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Ig kappa chain V-II region TEW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21,
21,
26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 2:
01-JUN-2002 (TrEMBLrel. 2:
01-MAR-2004 (TrEMBLrel. 2:
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                 23
39
54
61
102
112
                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                        PIR; A90370; K2HUTW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          24
40
55
62
103
113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mar
Local Sim-
87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8TCD0
Q8TCD0;
                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
Q8TCD0
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                   80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                              1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DVVMTQSPLSLPVTLRQPASISCRSSQSPVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRD 60
                                                                                                                         1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                      SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                           "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531; M. X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                    78.2%; Score 465; DB 2; Length 240; 77.9%; Pred. No. 2.3e-40; Live 9; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 114;
                                                                                                                                                                                                                                                        01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 78.0%; Score 464; DB 2; Length 11 Best Local Similarity 77.9%; Pred. No. 1.2e-40; Matches 88; Conservative 13; Mismatches 12; Indels
                                        Hypothetical protein. - SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL, AF035034; AAD56270.1; --
PIR; B49002; B49002.
PIR; S23638; S23638.
PIR; S34094; S34094.
PIR; S34095; B34095.
HSSP; P016Z5; ILVW.
InterPro; IPR007110; Ig-like.
InterPro; IRR003596; Ig-v.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z
                                                                                                                                                                                                                             114 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113
        SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KV2D HUMAN STANDARD;
P01617;
21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROSITE, PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13,
                                                                               Local Similarity 77.9 les 88; Conservative
 SMART; SM00407; IGc1; 1.
                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                         Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
NON TER
SEQUENCE
                                                                                                                                                     61
                                                                                                                                                                         81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                      fetus.";
                                                                     Query Match
                                                                                                                                                                                                                                      09UL80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
KV2D_HUMAN
                                                                                 Best Loc
Matches
                                                                                                                                                                                                       RESULT S
                                                                                                                                                                                                                  09UL80
 8 X R R R S
                                                                                                                                 g
                                                                                                                                                     δ
                                                                                                                                                                         g
                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 E
                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઢ
```

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                               "Structural identity of Bence Jones and amyloid fibril proteins in a patient with plasma cell dyscrasia and amyloidosis.";
J. Clin. Invest. 52.1276-1281(1973).

-!- MISCELLANEOUS: The major amyloid protein appears to be identical with the Bence Jones protein isolated from the same patient.

-!- MISCELLANEOUS: This protein isolated from the urine of a patient with plasma cell dyscrasia and amyloidosis.

-!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                               οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYXCMZALQA-PITFGGGTRLEIK 112
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                 SEQUENCE (BENCE-JONES PROTEIN TEW).
MEDLINE=74148480; PubMed=4596149;
Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
"Amino acide acquence of a kappa Bence Jones protein from a case primary amyloidosis.";
Biochemistry 12:3763-3780(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.9%; Score 463.5; DB 1; Length 113; 77.0%; Pred. No. 1.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complementarity-determining-3.
                                                                                                                                                                                                                                                      [2]
MEDLINE=73166638; PubMed=4700495;
MEDLINE=73466638; PubMed=4700495;
Terry W.D., Page D.L., Kimura S., Isobe T., Osserman B.F., Glenner G.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12316 MW; 0C3C38F81F1843CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Framework-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Framework-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Framework-4
```

ä

```
RC TISSUE-Skin;

WEALINE-ZEASURS.

RA MISCINES.

RIA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIA Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,

RA Didchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Didchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Didchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robark S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Sarches R.A.,

Raber J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 DIVMTQTPLSSPVTLGQPASISCRSSESLLHSNGNTYLSWLHQRPGQPPRLLIYKISNRF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVVWTQTPLSLPVTPGEPASISCRSSOSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQVSHF-PRTFGGGTRVEIK 132
            Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCG63599; AAH63599.1; -.
HSSP; P01837; 1KCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 procein. -
239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
1G Kappa chain V-II region GM607 precursor (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Match 76.6%; Score 455.5; DB 2; Local Similarity 75.2%; Pred. No. 2.2e-39; les 85; Conservative 15; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR003599; Ig.
Interpro; IPR007110; Ig-11ke.
Interpro; IPR003597; Ig c1.
Interpro; IPR003596; Ig whC.
Interpro; IPR003596; Ig v.
Pfam; PF07654; C1-8et; I.
SMART; SM00407; IG1; I.
SMART; SM00407; IG21; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                  Mammalia; Eutheria;
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
SEQUENCE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KV2E HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
KV2E_HUMAN
         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCC SE LILIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                       TISSUE-LUNG;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

WETAUSDEOFR R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rataushorg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Roak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Garcia A.M., Cabber B.D.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rateeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rategiquez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and manalysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 DVVMTQSPLSLFVTLGQPASISCRSTQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
  Chordata; Craniata; Vertebrata; Buteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg_R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022362; AAH22362.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239 AA; 26234 MW; FACEDC3A3B03871D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Match 77.7%; Score 462.5; DB 2 Local Similarity 78.8%; Pred. No. 4.1e-40; les 89; Conservative 13; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, PO1834; 117Z.
InterPro; IRRO07110; 19-like.
InterPro; IPR007110; 19-like.
InterPro; IPR003597; 19_c1.
InterPro; IPR003596; 19_WHC.
Pfan; PF07654; C1-set; 1
SWART; SW00406; 1Gv; 1.
PROSITE; PS00289; 1G_MHC; UNKNOWN_1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR, S34095, S34095.
PIR, S40324, S40324.
PIR, S40374, S40374.
PIR, S42267, S42267.
PIR, S42268
Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S22658; S22658
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISSUE=Lung
```

1

Gaps

۲,

Length 239; Indels 9

113

81

Q6P491 Q6P491;

RESULT 8
Q6P491
ID Q6P4
AC Q6P4
AC Q6P4
DT 0S-J
DT 0S-J
DE HYPO
OS HOMO

SEQUENCE Query Match

Best Loca Matches

g ò

ò a Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiteh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHW-SWTFGQGTKVEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain V-II region RPMI 6410.
Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Prostate; MbMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.2%; Score 453.5; DB 1; Length 133; 77.9%; Pred. No. 1.8e-39; ive 13; Mismatches 11; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complementarity-determining-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14707 MW; 513CCAF3673009EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                           EMBL, Z00020, CAA77315.1, -.
PTR, A01890, KZHURP.
HSSP, Q99M37, 1191.
GO, GO:0005576, C:extracellular, NAS.
GO, GO:0005955, P:immune response; NAS.
InterPro, IPR007100, IG-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Framework-3
  Nucleic Acids Res. 13:6499-6513(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00047; ig, i. —
MARAT; SM00406; IGV; I. PROSITE; PSS0835; IG LIKE; I. Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MRR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8NEKO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBNEKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
  SOUTH THE TENT THE TE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                        MEDLINE=84191506; PubMed=6325927;
Klobeck H.G., Solomon A., Zachau H.G.;
"Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kappa chain V-II region GM607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.2%; Score 453.5; DB 1; Length 117; 77.9%; Pred. No. 1.6e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complementarity-determining-1.
Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complementarity-determining-2. Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complementarity-determining-3. Framework-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12664 MW; 92C57DC719E558B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-II region RPMI 6410 precursor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005576; C:extracellular; NAS. GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS. InterPro; IPR007110; IG-like.
                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z00009; -; NOT_ANNOTATED_CDS.
PIR; A01889; K2HUGM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig. 1.
SMART; SM00406; IG; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V regIon; Signal.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                              diversity.";
Nature 309:73-76(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                       Q99M37; 119I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
hes 88; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia, Euther;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KV2F HUMAN
P06310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

80

Gaps

;

φ

```
Local Similarity 76.3% les 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                   115
                        B91639; K2HUCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KV2B HUMAN P01615;
                                                                                                                                                                                                                                                                                                                                                                                                NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct |
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KV2B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                        DAR WENT TO SEE THE SECOND SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Yrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIVMTOSPLSLPVTPGEPASISCRSSQSLLHSDGYNYLDWYLQKPGQSPQLLIYLGSNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular basis of antibody formation.";
Naturwissenschaften 56:195-205(1969).
-!- MISCELLANBOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANBOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hilschmann N , , "The complete amino acid sequence of Bence Jones protein \operatorname{Cum} (kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.,
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC030814, AAH30814.1, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 239 AA; 26024 MW; FSE20AD3B0552COA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.1%; Score 452.5; DB 2
Best Local Similarity 76.1%; Pred. No. 4.6e-39;
Matches 86; Conservative 12; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
15 kappa chain V-II region Cum.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1] —
SEQUENCE.
MEDLINE=68242259; PubMed=5586923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS TO 50; 52; 96 AND 97.
MEDLINE=70063440; PubMed=4188189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig_cl.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
Pfam; PR07654; Cl-set; I.
SMART; SM00406; IGv; I.
                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S40342; S40342.
PIR; S40357; S40357.
HSSP; P01834; 1172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S23638; S23638
PIR; S34091; S34091
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hilschmann N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KV2A HUMAN
P01614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
KV2A_HUMAN
```

g ò

ò

```
59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                        DVVMTQTPLSLPVTPGEPASISCRSSQSLVHR-NGNTYLHWYLQKPGQSPKLLIHKVSNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riesen W.F., Jacon J.-C.;
"Variable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine.";
Biochemistry 15:3829-3831(1976).
I- MISCELLANEOUS: This of hain was isolated from a Waldenstrom's macroglobulin that binds phosphorylcholine.
PIR; A01886; KZHUFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 ASGVPDRFSGSGSGTDFTLKISRVQAEDVGVYYCMQRLEI-PYTFGQGTKLEIR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                      ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.0%; Score 440.5; DB 1; Length 113;
                                                                                                                                                                                                                                                                                                                                          Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Framework-3.
Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complementarity-determining-1
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                          115 AA; 12676 MW; 59E9F90A379569EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OCODA39E46DB96BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF0047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 1. Direct protein sequencing; Immunoglobulin V region.
74.6%; Score 444; DB 1; L. 76.3%; Pred. No. 1.5e-38; ive 13; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
11g kappa chain V-II region FR.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Framework-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, 099M77, II91.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=76253627; PubMed=821524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12660 MW;
```

```
musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                   TER
                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                            ò
             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                          Dreyer W. J., Gray W. R., Hood L. B.;

The genetic, molecular, and cellular basis of antibody formation:
T some facts and a unifying hypothesis.;

Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).

-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.

-!- MISCELLANEOUS: This is a Bence-Jones protein.

R PIRSP: Q99M37; 1191.

R SPP Q99M37; 1191.

R InterPro; IPR00310; Ig-V.

R Pfam; PF00047; ig; 1.

R PROSITE; PS50835; IG_LIKE; 1.

R Bence-Jones protein; Direct protein sequencing;

W Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
            1; Gaps
                                                                                                                                                                                                                                                                                                                     marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Gaps
                                                                       61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYPCSQSTHVPPLTFGAGTKLELK 113
                                                                                  61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Complementarity-determining-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complementarity-determining-3
          14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12055 MW; E5B22E2FA7ABE481 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.6%; Score 426; DB 1;
69.0%; Pred. No. 1.1e-36;
ive 21; Mismatches 12,
 Pred. No. 3.4e-38;
                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
19 kappa chain V-II region 7834.1.
          13; Mismatches
                                                                                                                                              112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Framework-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Framework-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Framework-2
                                                                                                                                              PRT;
                                                                                                                                                                                               Ig kappa chain V-II region MIL.
Homo sapiens (Human).
 75.2%;
          85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
tes 78; Conserv
                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                              KV2C_HUMAN
P01616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KV2F_MOUSE
                                                                                                                                                                                                                                                      [1]
SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
KV2F MOUSE
                                                                                                                                   KV2C HUMAN
          Matches
                              ઠે
                                                                       ò
                                                                                        셤
                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
```

```
MEDLINE=83256427; PubMed=6409088;

WEDLINE=83256427; PubMed=6409088;

WEDLINE=83256427; PubMed=6409088;

The Chains Grown a mouse hybridoma-derived anti-(streptococcal group and a polysaccharide) antibody containing an additional cysteine residue. The polysaccharide antibody against the streptococcal group A polysaccharide.

The corresponding against the streptococcal group A polysaccharide.

The A01913; KWMS7S.

PIR; A01913; KWMS7S.

HSSP; Q99M37; 1191.

InterPro; IPR001110; Ig-like.

InterPro; IPR001110; Ig-like.

InterPro; IPR001596; Ig_v.

PRART; SM0406; IGv; I.

SMART; SM0406; IGv; I.

RW SNART; SM0406; IGLIKE; I.

WM Direct protein sequencing; Hybridoma; Immunoglobulin V region;

WM Monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SGVPDRFSGSGSGTAFTLRISRVEAEDVGVYYCMQQREY-PYTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SGVPDRFSGSGSGTDFTLKISRVBABDLGVYFCSQSTHVPPLTFGAGTKLBLK 113
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Framework-1.
Complementarity-determining-1.
Framework-2.
Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12496 MW; 42C019D10ADA3C91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 1.1e
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.0%; Score 416.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Framework-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: April 18, 2005, 10:03:55 Job time : 85.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 70.8
les 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
39
54
61
61
102
93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 AA;
                                                         NCBI_TaxID=10090;
```

This Page Blank (uspto)

```
(without alignments)
536.541 Million cell updates/sec
                                                                                                                                                           1 DVVMTQTPLSLPVTPGEPAS.....SQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                        April 18, 2005, 10:04:06; Search time 70 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:
/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                              1421835 segs, 332370683 residues
                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                 US-10-737-208A-1
595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                        Scoring table:
                                                                                                                                                               Sequence:
                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	19, App	20, Ap	17, App	18, Ap	, Appl	'5, App	06, Ap	Appl	, Appl	, Appl	, Appl	15, App	16, Ap
ជ	9	ž	9	ñ	ä	6	ñ	99	ĕ	ñ	č	8	ñ
Description	Sequence	Sequence	Sequence 687, App	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Seguence	Sequence 2016, Ap
ID	US-10-468-370-689	US-10-468-496-2020	US-10-468-370-687	US-10-468-496-2018	US-10-762-629-18	US-10-468-370-675	US-10-468-496-2006	JS-09-753-436-66	US-10-163-942-66	US-10-372-481-29	US-10-371-797-29	US-10-468-370-685	US-10-468-496-2016
80	15	16	15	16	16	12	16	ω _	14	12	15	12	16
% Query : Match Length DB	113	113	113	113	114	113	113	116	116	139	139	113	113
% Query Match	95.8	95.8	93.8	93.8	91.9	89.4	89.4	89.5	89.5	89.0	89.0	88.4	88.4
Score	570	570	558	558	547	532	532	530.5	530.5	529.5	529.5	526	526
Result No.		7	m	4	2	9	7	æ	6	10	11	12	13

22,	4 Sequence 14,	Sequence 35,	Sequence 42,	O Sequence 20,	Seguence 47,	Seguence 48,	Seguence 4	3 Sequence 683	14 Sequence	Sequence	Sequence	Seguence 4	Sequence	Sequence	Sequence	Sequence 2012	Seguence	Sequence 2010	3, Ap	Sequence	7 Sequence 67	Sequence 20	Sequence 95	Sequence 2,	Sequence 45,	Seguence 26,	7	Sequence 6, Appli	Seguence 10,	Sequence 85,	Sequence 87,
nS	US-10-741-657A-	Sn	US-09-726-258-4	ns	US-10-239-656-4	US-10-239-656-4	5 US-10-239-656-49	US-10-468-370	US-10-468-4	US-09-518-737-4	US-10-723-7	US-09-887-853-4	_	_	_	6 US-10-468-496-2012	_	_	US-10-270-555	10-687-035	US-10-468-370	US-10-468-496-2	US-09-947-839-	US-10-388-214A-	US-09-726-258-4	US-10-258-728-2	US-10-919-	US-10-	US-10-138-505-	US-10-257-864A	S US-10-257-864A-87
-	-	٦	-	-	H	~	٦	-	-	-	-	2	-	-	-	-	_	m	Н	-	-	-		н	-	Ч	Ч	٦	-	_	1 15
112	11	13	24	11	50	51	51	11	11	11	11	25	13	25	11	11	11	11	47	131	11	11	13	13	11	11	11	13	13	13	13
88.3	88.0	88.0	88.0	87.8	87.8	87.8	87.8	87.4	87.4	87.1	87.1	87.1	87.0	9.98	9.98	9.98	86.1	86.1	96.0	85.6	85.4						84.8	84.8	84.8	84.8	84.8
525.5	523.5	523.5	523.5	522.5	522.5	522.5	522.5	520	520	518.5	518.5	518.5	517.5	515.5	515	515	512	512	511.5	509.5	508	508	507.5	507.5	905	504.5	504.5	504.5	504.5	504.5	504.5
14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
US-10-468-370-689

US-10-468-370-689

Sequence 689, Application US/10468370

PUDLication No. U320040082039A1

GENERAL INFORMATION:

APPLICANT: Gallies, Stephen

APPLICANT: Gallies, Stephen

APPLICANT: Garter, Graham

APPLICANT: Hamilton, Anita

APPLICANT: Hamilton, Anita

APPLICANT: Walkins John

APPLICANT: Watkins Lib

FRICK APPLICATION NUMBER: EP 01103955.9

FRICK FILING DATE: 2001-04-05

PRICK APPLICATION NUMBER: EP 01103955.9

FRICK FILING DATE: 2001-04-05

FRICK FILING DATE: 2001-
```

```
US-10-468-370-687
                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | SAPELICANT: Carr. Francis J. |
| APPLICANT: Jones, Tim |
| APPLICANT: Jones, Tim |
| APPLICANT: Jones, Tim |
| APPLICANT: Hamilton, Anita |
| APPLICANT: MAUNITON: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED |
| TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED |
| TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED |
| TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED |
| TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED |
| FRIOR PRILING DATE: 2001-03-02 |
| PRIOR PRILING DATE: 2001-03-15 |
| PRIOR PRILING DATE: 2001-03-20 |
| PRILING DATE: 2001
          ö
                                                                                                                     1 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRP
                                                                 1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DVVWIQTPLSLPVSLGDQASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                     SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                             61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

95.8%; Score 570; DB 16; Length 113;
Best Local Similarity 96.5%; Pred. No. 1.6e-45;
Matches 109; Conservative 2; Mismatches 2; Indels
          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: MHC class II binding epitope
   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 687, Application US/10468370; Publication No. US20040082039A1; GABERAL INFORMATION:
APPLICANT: Garr, Francis J.
APPLICANT: Carr, Francis J.
APPLICANT: Carrer, Graham
APPLICANT: Hamilton, Anita
APPLICANT: Williams, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2020, Application US/10468496
Publication No. US20040180386A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
   109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-468-496-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-10-468-370-687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
Matches
                                                                                                                                a
                                                                     à
                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
```

```
APPLICANT: Watter, John APPLIC
```

?

```
IMMUNOGENICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-468-496-2006
                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                     1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                 1 DVVMTQTPGSLPVSAGDQASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                             SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                      SGVPDRFSGSGSGTDFTLKISRVEAEDSGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ## STENERAL INFORMATION:
## APPLICANT: Abdel-Meguid, Sherin
## APPLICANT: Ho, Yen Sen
## TITLE OF INVENTION: Recombinant IL-18 Antagonists Useful in
## TITLE OF INVENTION: Treatment of IL-18 Mediated Disorders
## TITLE OF INVENTION: Treatment of IL-18 Mediated Disorders
## TITLE OF INVENTION: Treatment of IL-18 Mediated Disorders
## CURRENT APPLICATION NUMBER: US/09/914,695
## RIOR PELLOR DATE: 2001-08-31
## PRIOR PELLING DATE: 2000-03-17
## PRIOR FILING DATE: 2000-03-17
## PRIOR FILING DATE: 1999-03-19
## NUMBER OF SEQ ID NOS: 48
## SOFTWARE: FastSEQ for Windows Version 4.0
## SEQ ID NO 18
## ELENCTH: 114
                                                              Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 547; DB 16; Length 114;
Pred. No. 2.3e-43;
4; Mismatches 5; Indels
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hanlon, Marian
APPLICANT: Watkins, John
APPLICANT: Baker, Matthew
APPLICANT: Bay, Jeffrey
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
                                                              Score 558; DB 16;
Pred. No. 2.1e-44;
2; Mismatches 4;
OTHER INFORMATION: MHC class II binding epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 675, Application US/10468370
Publication No. US20040082039A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Carr, Francis J.
APPLICANT: Jones, Tim
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/10762629
Publication No. US20040141964A1
GENERAL INFORMATION:
                                                           Query Match 93.8%;
Best Local Similarity 94.7%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

Best Local Similarity 92.0%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carter, Graham
Hamilton, Anita
Williams, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus musculus
    ; US-10-468-496-2018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-468-370-675
                                                                                                                                                                                                                                                                                                                                                                         US-10-762-629-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-762-629-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                     ઠ
                                                                                                                                                                                             요
                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
```

```
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: IMMUNOGENCITY
FILE REFERENCE: MER-117
CURRENT APPLICATION NUMBER: US/10/468,496
CURRENT FILING DATE: 2003-09-25
FRIOR APPLICATION NUMBER: U13954.2
FRIOR RILING DATE: 2001-02-19
FRIOR FILING DATE: 2001-03-08
FRIOR FILING DATE: 2001-03-08
FRIOR PAPLICATION NUMBER: 01106538.0
FRIOR PAPLICATION NUMBER: 01106536.4
FRIOR APPLICATION NUMBER: 01106536.4
FRIOR APPLICATION NUMBER: 0110636.4
FRIOR APPLICATION NUMBER: 0110636.4
FRIOR APPLICATION NUMBER: 0110636.4
FRIOR APPLICATION NUMBER: 0110636.4
FRIOR PILING DATE: 2001-03-15
FRIOR PILING DATE: 2001-03-15
FRIOR PILING DATE: 2001-03-20
FRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DVVWTQSPGTLPVSLGERATISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SGVPDRFSGSGSGTDFTLTISRLEAEDLAVYFCSQSTHVPPLTFGQGTKLEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 89.4%; Score 532; DB 15; Best Local Similarity 89.4%; Pred. No. 5.6e-42; Matches 101; Conservative 6; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.4%; Score 532; DB 16;
89.4%; Pred. No. 5.6e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: MHC class II binding epitope US-10-468-370-675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THER INFORMATION: MHC class II binding epitope
CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT FILING DATE: 2003-08-19
PRIOR PILLING DATE: 2003-08-19
PRIOR FILLING DATE: 2001-02-19
PRIOR PILLING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR APPLICATION NUMBER: P01/EP02/01690
PRIOR PILLING DATE: 2002-02-18
NUMBER: PREQIB NOS: 689
SEQ ID NO 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 2036
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-468-496-2006; Sequence 2006, Application US/10468496; Publication No. US20040180386A1; GENERAL INFORMATION: APPLICANT: Carter, Graham; APPLICANT: Jones, Tim APPLICANT: Jones, Tim APPLICANT: Williams, Stephen; APPLICANT: Williams, Stephen; APPLICANT: Hamilton, Anita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
```

Gaps

1;

```
1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                           5 DIVMIQSPLSLPVIPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF
                                                                                                                                                                                                                                                                   SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                             65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHV-PYTFGQGTKVEIK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois COUNTRY: United States of America ZIP: 6060-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
                                                               Score 530.5; DB 9; Length 116;
Pred. No. 7.9e-42;
9; Mismatches 3; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/753,436
FILING DATE: «Unknown»
APPLICATION NUMBER: 09/382,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: «Unknown»
PEDLICATION NUMBER: US 08/487,113
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/286,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/102,852
ELING DATE: 05-AUG-1993
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/163,942
FILING DATE: 05-5un-2002
CLASSIFICATION: vUNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 26-MAY-1992
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/889,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., C
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 66, Application US/10163942
Publication No. US20030199423A1
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (312) 474-0448
                                                            Query Match
Best Local Similarity 88.5%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
          US-09-753-436-66
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-10-163-942-66
                                                                                                                                                                                                              g
                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                             셤
          ö
                                                                                 1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
          0; Gaps
                                                                                                                                                                                   61 SGVPDRFSGSGSGTDFTLTISRLEAEDLAVYFCSQSTHVPPLTFGQGTKLEIK 113
                                                                                                                                                      SGVPDRFSGSGSGTDFTLKISRVBAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gallatin, W. Michael
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: 1CAM-Related Materials and Methods
TITLE OF INVENTION: 1.20
CORRESPONDENCE: 1.20
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/753,436
     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/382,289
FILING DATE: 07-UTN-1995
FILING DATE: 07-UTN-1995
FILING DATE: 07-UTN-1995
FILING DATE: 05-AUG-1994
FILING DATE: 05-AUG-1994
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
FILING DATE: 22-JAN-1993
FILING DATE: 22-JAN-1993
FILING DATE: 05-UN-1992
FILING DATE: 05-UN-1992
FILING DATE: 05-UN-1992
FILING DATE: 05-UN-1992
FILING DATE: 20-UN-1992
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-UN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPAX: (312) 474-6300
TELEFAX: 25-8856
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             Sequence 66, Application US/09753436
Patent No. US20010029293A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
     101;
Matches
                                                  ð
                                                                                               ద
                                                                                                                                                    ò
                                                                                                                                                                                                 셤
```

?

ઠે 요 g

ઠ

```
US-10-468-496-2016
; Sequence 2016, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hamilton, Anita
Williams, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gillies, Stephen APPLICANT: Carr, Francis J. APPLICANT: Jones, Tim APPLICANT: Carter, Graham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanlon, Marian
                                              ; ORGANISM: homo sapiens
US-10-371-797-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 685
    LENGTH: 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   요
                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/10372481
; Sequence 29, Application US/10372481
; Publication No. US20030202975A1
; GENERAL INFORMATION:
    APPLICANT: Tedder, Thomas F.
    TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
; FILE REFRENCE: 5405.306
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/10/372,481
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR FILING DATE: 2002-10-21
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; LEWGTH: 139
; TYPE: PRI
                                                                                                                                                              1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                           1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 79
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                          61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHV-PYFFGGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                    ä
                                                                    DB 14; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 15; Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 29, Application US/10371797
Fublication No. US20040001828A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: TEDDER, Thomas
TILLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 39754-0951
FILE REFERENCE: 39754-0951
CURRENT FILING DATE: 2003-02-21
PRIOR FILING DATE: 2003-02-21
PRIOR PLICATION NUMBER: US 60/420,472
PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2002-10-21
PRIOR FILING DATE: 2002-10-21
SPIOR APPLICATION NUMBER: US 60/359,419
FRIOR FILING DATE: 2002-02-11
SPIOR PELICATION NUMBER: US 60/359,419
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FREEER FREECY FOR WINDOWS VERSION 4.0
                                                                 Score 530.5; DB 14;
Pred. No. 7.9e-42;
9; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 89.0%; Score 529.5; DB 15; Best Local Similarity 91.2%; Pred. No. 1.2e-41; Matches 103; Conservative 4; Mismatches 5;
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-163-942-66
                                                                 Query Match
Best Local Similarity 88.5%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-372-481-29
                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-10-372-481-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
```

g

ठे

g ઠે

```
9
                                                                                                                                                          20 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 79
                                                                                                           1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Query Match 89.0%; Score 529.5; DB 15; Length 139; Best Local Similarity 91.2%; Pred. No. 1.2e-41; Matches 103; Conservative 4; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THER INFORMATION: De-immunized MHC class II binding epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

88.4%; Score 526; DB 15; Length 1:
Best Local Similarity 86.7%; Pred. No. 2e-41;
Matches 98; Conservative 9; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Matkins, John
APPLICANT: Baker, Matthew
APPLICANT: Baker, Matthew
APPLICANT: Way, Jeffrey
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
TITLE OF INVENTION: IMMUNOGENICITY
FILE REPERROR: MER-118
CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT PILING DATE: 2003-08-19
FRIOR FILING DATE: 2001-02-19
PRIOR FILING DATE: 2001-02-19
PRIOR PPLING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: PCT/EP02/01690
PRIOR FILING DATE: 2002-02-18
PRIOR FILING DATE: 2002-02-18
NUMBER OF SEQ ID NOS: 689
SOFTWARE PRESENCE OF WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 685, Application US/10468370 Publication No. US20040082039A1 GENERAL INFORMATION:
```

```
TYPE: PRT
ORGANISM: Mus sp.
                                                                                                                RESULT 15
US-10-741-657A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-741-657A-14
           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                         APPLICANT: Williams Stephen
APPLICANT: Williams Stephen
APPLICANT: Williams Stephen
APPLICANT: Williams Stephen
APPLICANT: Hamilton, Anita
ITILE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
ITILE OF INVENTION: EPITODES AND USE FOR PREPARING MOLECULES WITH REDUCED
ITILE OF INVENTION: IMMUNGERINTY
FILE OF INVENTION: IMMUNGER: US/10/468,496
ITILE APPLICATION NUMBER: 01103954.2
PRIOR APPLICATION NUMBER: 01103954.2
PRIOR APPLICATION NUMBER: 0110577.5
PRIOR APPLICATION NUMBER: 01106538.0
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-03-15
PRIOR PILING DATE: 2001-03-20
PRIOR FILING DATE: 2001-03-20
PRIOR FILING DATE: 2001-03-20
PRIOR PLING DATE: 2001-03-20
PRIOR FILING DATE: 2001-03-20
PRIOR SPLING DATE: 2001-03-20
PRIOR SPLING DATE: 2001-03-20
PRIOR PILING DATE: 2001-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DVVMTQSPGTLPVSLGBRATISCRSSQSLVHRNGNTYLHWYLQKPGQSPKMLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVWMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGVPDRFSGSGSGTDFTLTISRLEAEDMAVYFCSQSTHVPPLTFGGGTKVEIK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.4%; Score 526; DB 16; Length 113; 86.7%; Pred. No. 2e-41; 1.ve 9; Mismatches 6; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-10-741-657A-22
is Sequence 22, Application US/10741657A
is Publication No. US20040197325A1
is GENERAL INFORMATION:
if TITLE OF INVENTION: ANTIBODIES AGAINST GPR64 AND USES THEREOF
if TITLE OF INVENTION: ANTIBODIES:
if TITLE REPERENCE: 05882.0177.NPUS01
if CURRENT APPLICATION NUMBER: US/10/741,657A
if UNBER OF SEQ ID NOS: 30
if NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 525.5; DB 16;
Pred. No. 2.2e-41;
5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-496-2016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin version 3.2
SEQ ID NO 22
LENGTH: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 88.3%;
Best Local Similarity 90.3%;
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 86.78
Matches 98; Conservative
Graham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Mus
US-10-741-657A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
| Besture | Best
```

```
Sequence 4, Application US/09232290A
Patent No. 6815540
GENERAL INFORMATION:
APPLICANT: PLUCKTHUN, ANDREAS
APPLICANT: PLUCKTHUN, ANDREAS
APPLICANT: HONEGGER, ANNEWARIE
APPLICANT: HONEGGER, ANNEWARIE
TITLE OF INVENTION: INMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
FILE REFERENCE: MORPHO/7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 104; Conservative
                            2242
22422
22522
22338
22338
22388
22388
22388
23388
23388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 1
US-09-914-695-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-914-695-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-09-232-290-4
523.5
523.5
523.5
523.5
523.5
518.5
518.5
518.5
518.5
518.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
517.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, App]
                                                                                                                        (without alignments)
443.965 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56,
56,
42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
                                                                                                                                                                                              1 DVVMTQTPLSLPVTPGEPAS......SOSTHVPPLTFGAGTKLELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                      April 18, 2005, 09:57:36; Search time 19 Seconds
                                                                                                                                                                                                                                                                                                           513545
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-232-290-4
US-08-482-882-66
US-08-483-99-66
US-08-473-503-66
US-08-773-503-66
US-08-713-503-66
US-08-714-017-66
US-08-714-017-66
US-08-714-017-66
US-08-798-939-7
US-08-99-939-7
US-08-998-613A-48
US-08-998-613A-48
US-08-998-613A-48
US-08-998-613A-48
US-08-98-613A-48
US-08-98-613A-48
US-08-98-613A-48
US-09-027-449-35
US-09-027-449-35
US-09-027-443-35
US-09-021-923A-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-398-613A-56
US-08-398-612A-56
US-08-398-611A-56
US-08-491-334A-56
US-09-027-449-42
                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                             513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         - protein search, using sw model
                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                US-10-737-208A-1
595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                     score:
                                                                         OM protein
                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                  Perfect
                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
```

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                               Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SGVPDRPSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                    Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/09914695

Patent No. 6706487

GENERAL INFORMATION:
APPLICANT: Abdel-Meguid, Sherin
APPLICANT: Ho, Yen Sen
APPLICANT: Ho, Yen Sen
TITLE OF INVENTION: Recombinant IL-18 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL-18 Mediated Disorders
TITLE OF INVENTION: Treatment of IL-18 Mediated Disorders
TITLE OF INVENTION: Treatment of IL-18 Mediated Disorders
FILE REFERENCE: P50897

CURRENT APPLICATION UNMBER: US/09/914,695

CURRENT FILING DATE: 2000-08-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 1999-03-19

NUMBER OF SEQ ID NOS: 48

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.9%; Score 547; DB 4; Length 114; 92.0%; Pred. No. 7.4e-46; ive 4; Mismatches 5; Indels
US-08-804-444A-42
US-09-026-985-42
US-09-0121-952A-42
US-09-0131-952A-42
US-08-133-341-7
US-08-133-804-4
US-08-461-386-4
US-08-461-386-4
US-08-461-386-4
US-08-257-341-5
US-08-257-341-5
US-08-926-789-12
US-09-166-093-21
US-09-166-093-21
US-09-166-093-21
US-09-166-093-21
US-09-166-093-21
US-09-166-093-21
US-09-166-093-21
US-09-166-093-21
US-09-166-093-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
```

ö

```
89.2%;
               (312) 474-0448
                                                                                               : 116 amino acids
amino acid
                          TELEX: 25.3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 116 amino acid
                                                                                                                                                                                                                                       Best Local Similarity 88.5
Matches 100; Conservative
                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-882-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Suh, Young J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-483-389-66
             TELEFAX:
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                     1 DVVWIQIPLSLPVSLGDQASISCRSSQSLVHSNGNIYLHWYLQKPGQSPKLLIYKVSNRF 60
                                                                                                                                                                                                                                                                                                                                         1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SGVPDRFSGSGSGTDFYLKISRVEAEDLGVYFCSQSTHV-PLTFGAGTKLELK 112
                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                             Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-482-865
US-08-482-865
Sequence 66, Application US/08482882
Patent No. 5773218
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: 116AM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maraball, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRIES 60606

ZIFF. 60606

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,882
FTI.NG DATE: 07-JUN-1995
                                                                                                                                                                                                                                                         Score 533.5; DB 4;
Pred. No. 1.5e-44;
3; Mismatches 4;
CURRENT APPLICATION NUMBER: US/09/232,290A CURRENT FILING DATE: 1999-01-15 EARLIER APPLICATION NUMBER: PCT/EP96/02230 EARLIER FILING DATE: 1996-05-23 NUMBER OF SEQ ID NOS: 60 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-JAN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-UN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGBNT INFORMATION:
NAME: NO. 5773218and, Greta E.
REGISTRATION NUMBER: 35,3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 08/102,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JMBER: US 08/009,266
22-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 32178 IELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: US 08/
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
                                                                                                                                                                                                                                                         89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (312) 474-6300
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 92.98
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 Sear
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Murine
US-09-232-290-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                     113
                                                                                                                             SEQ ID NO 4
                                                                                                                                                     LENGTH
                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
5 DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF
                                                                                                                                       1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                            Gaps
                                                                                                                                                                                                                                                                                 61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                         SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHV-PYTFGQGTKVEIK 116
                                                                        1;
Score 530.5; DB 1; Length 116; Pred. No. 3e-44;
                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALDRESSER: AGISTALI, O'TOOLE, GERBLEIN, MULTARY ENTREET: 233 SOUTH WACKET DIIVE/6300 Sears TOWER STATE: Illinois
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
21P: 60606
COMPUTER READBALE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,389
FILING DATE: U-JUN-1995
CLASSIPICATION NUMBER: US 08/102,852
FILING APPLICATION NUMBER: US 08/102,852
FILING APPLICATION NUMBER: US 08/009,266
FILING APPLICATION NUMBER: US 07/894,061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                     9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 66, Application US/08483389
Patent No. 5811517
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-RELATED PROTEIN
NUMBER OF SEQUENCES: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: P-41,337
REFERENCE/DOCKET NUMBER: 27866/
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: (312) 474-6448
TELEFAX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
```

Gaps

1;

```
1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                    5 DIVWTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                               SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSGSTHVPPLFFGAGTKLELK 113
                                                                                                                                                                        Query Match 89.2%; Score 530.5; DB 2; Length 116; Best Local Similarity 88.5%; Pred. No. 3e-44; Matches 100; Conservative 9; Mismatches 3; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marehall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-473-503-66

Sequence 66, Application US/08473503

Sequence 66, Application US/08473503

Sequence 10. 5865262

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
ITILE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: POEDM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
COMPUTER: IRM PC compatible
COMPUTER: IRM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,503
FILING DATE: 07-UUN-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 25-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-AUN-1992
PRIOR APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-AUN-1992
PRIOR APPLICATION NUMBER: US 07/889,724
FILING DATE: 27-JAN-1992
RIUNG DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5869262and, Greta E.
REGISTRATION NUMBER: 33,302
REGISTRATION NUMBER: 33,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPERENCE/DOCKET NUMBER: 3217
RELECOMMUNICATION INFORMATION:
TELEFORE: 312, 474-6300
TELEFORE: 312, 474-6448
TELER: 25-3856
INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
LEUNTH: 116 antho acids
TYPE: amino acid
                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-113D-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDA...
STREET: 65...
CITY: Chicago
       amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                    1 DVVWTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                          Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 66, Application US/08487113D

Patent No. 5837822

GENERAL INPORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay

TITLE OF INVENTION: ICAM-Related Materials and Methods
ITITLE OF INVENTION: ICAM-Related Materials and Methods

NUMBER OF SEQUENCES: 120

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 6606-6402

COUNTRY: United States of America
ZIP: G606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPUTER: IBM
                                                                                                                                                                                                    Length 116;
                                                                                                                                                                                                 Score 530.5; DB 2;
Pred. No. 3e-44;
9; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,113D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DAMBER: US 07/894,061
PILING DATE: 05-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-UAN-1992
ATTORNEY/AGENT INFORMATION:
NAMBE: NO 5837822and, Greta E.
REGISTRATION NUMBER: 35,302
RECISTRATION NUMBER: 35,302
RECISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEFAX: (312) 474-6448
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                 Query Match 89.2%;
Best Local Similarity 88.5%;
Matches 100; Conservative
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 amino acids
                                                                                           , MOLECULE TYPE: protein US-08-483-389-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-487-113D-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

```
FILING DATE:
                                                                                                                                                                                                 엄
                                                                                                                                              ð
                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                           1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                             5 DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF
                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                            61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                              89.2%; Score 530.5; DB 2; Length 116; 88.5%; Pred. No. 3e-44; Live 9; Mismatches 3; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 66, Application US/08483932
Patent No. 5880268
GENERAL INPORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
INVERSE OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Galo Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,932

FILNG DATE: US/08/483,932

FILNG DATE: US/08/483,932

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/102,852

PILING DATE: 05-AUG-1994

APPLICATION NUMBER: US 08/102,852

PRIOR APPLICATION NUMBER: US 08/102,852

PRIOR APPLICATION NUMBER: US 08/009,266

FILING DATE: 22-JAN-1993

PRIOR APPLICATION NUMBER: US 07/894,061

FILING DATE: 05-AUG-1993

PRIOR APPLICATION NUMBER: US 07/894,061

FILING DATE: 22-JAN-1992

PRIOR APPLICATION NUMBER: US 07/899,724

FILING DATE: 26-AWAY-1992

PRIOR APPLICATION NUMBER: US 07/889,724

FILING DATE: 26-AWAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: NO. 5880268and, Greta E.

REGISTRATION NUMBER: 35,3022

PREPERPRATION NUMBER: 35,3022

PREPERPRATION NUMBER: 35,3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32178
TELEPHONE: (312) 474-6500
TELEFAR: (312) 474-648
TELEFAR: 25-3856
INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
                                                                              Query Match
Best Local Similarity 88.5
Matches 100; Conservative
; MOLECULE TYPE: protein US-08-473-503-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-483-932-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                  유
```

```
1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                Gaps
                                                                                                                                                                                                        61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQSTHV-PYTFGQGTKVEIK 116
                                                        1;
Query Match

89.2%; Score 530.5; DB 2; Length 116;
Best Local Similarity 88.5%; Pred. No. 3e-44;
Matches 100; Conservative 9; Mismatches 3; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                           RESULT 8
US-08-720-420A-66
; Sequence 66, Application US/08720420A
; Patent No. 5989843
; GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
; TITLE OF INTENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,420A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRICHAGO NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009 266
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illingis
COUNTRY: United States of America
ZIP: 6060-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
RAPPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
REIOR PAPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
REIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,113
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Williams, Joseph A., Jr. REGISTRATION NUMBER: 38,659
REFERENCE DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
ITELEX: 25-3866
INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS: LENGTH: 116 amino acide
TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: 'amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6300 CITY: Chicago
```

```
1 DVVWTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                       5 DIVMTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRP
                                                                                                                                                                                                                                                                      65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSOSTHV-PYTFGQGTKVEIK 116
                                                                                                                                                                                                                                               61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 116;
                            Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 S. Wacker Drive
                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 66, Application US/08475680
Patent No. 6100383
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: 11linois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/475,680
FILING DATE: 07-UNN-1995
CLASSIFICATION: 530
                         89.2%; Score 530.5; DB 3;
88.5%; Pred. No. 3e-44;
ive 9; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.2%; Score 530.5; DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE: 05-AUG-1994
FILING DATE: 05-AUG-1993
FILING DATE: 05-AUG-1993
FILING DATE: 05-AUG-1993
FILING DATE: 22-JAN-1993
FILING DATE: 22-JAN-1993
FILING DATE: 22-JAN-1993
FILING DATE: 22-JAN-1993
FILING DATE: 05-UN-1992
FILING DATE: 05-UN-1992
FILING DATE: 05-UN-1992
FILING DATE: 26-MAY-1992
FILING DATE: 26-MAY-1992
FILING DATE: 27-JAN-1992
FILING DATE: 27-JAN-1992
FILING DATE: 27-JAN-1992
FILING DATE: 36-MAY-1992
FILING DATE: 37-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                         Query Match 89.2
Best Local Similarity 88.5
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-475-680-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
CITY: Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                    q
                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                       1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                      S DIVWTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRF
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                               SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                           SGVPDRFSGSGSGTDFTLKISRVEAEDVGYYYCSQSTHV-PYTFGQGTKVEIK 116
                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 66, Application US/08714017
; Patent No. 604076
; GENERAL INFORMATION:
APPLICANT: Callatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                                                                              Length 116;
                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,017
                                                                            Score 530.5; DB 2;
Pred. No. 3e-44;
9; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLICASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286,754
FILING DATE: 05-AUG-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 22-AUM-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-AUN-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/899,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-AN-1992
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6040176and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IELEFAX: (312) 474-6300
IELEX: 25-3856
INPORMATION FOR SEQ ID NO: 66: SEQUENCE CHARACTERISTICS: LENGTH: 116 Amit-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 3:
FELECOMMUNICATION INFORMATION
TELEPHONE: (312) 474-6300
                                                                            Query Match
Best Local Similarity 88.5%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 116 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-08-714-017-66

    MOLECULE TYPE: protein
US-08-720-420A-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-714-017-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                               8
```

```
1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DVVLTQTPLSLPVSLGGQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 DFVMTQTPLSLPVSLGDQASISCRASQSLVHSNGNTYLHWYLQKPGQSPKLLIYRVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPP-TFGGGTKLEIK 271
                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: Amino acid; OTHER INFORMATION: sequence for L49-sFV-bL including PelB leader US-09-070-637-20
                             APPLICANT: SIEMERS, NATHAN O.
APPLICANT: SENTER, SUGAN
APPLICANT: SENTER, DETER D.
TITLE OF INVENTION: RECOMBINANT ANTIBODY-ENZYME FUSION PROTEINS
FILE REPERENCE: 9197F-83.1
CURRENT APPLICATION NUMBER: US/09/070,637A
CURRENT PILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: 60/045,888
BARLIER PLILING DATE: 1997-05-07
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN Ver. 2.0
SEG ID NO 20
LENGTH: 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Process for Generating Specific Antibodies 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.4%; Score 526; DB 5; Length 218; larity 92.0%; Pred. No. 1.6e-43; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

88.5%; Score 526.5; DB 3; Length (
Best Local Similarity 89.4%; Pred. No. 4.5e-43;
Matches 101; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FULLOSYTIANOTOR
; Sequence 61, Application PC/TUS9414106
; GENERAL INFORMATION:
    APPLICANT:
; TITLE OF INVENTION: Process for Gener
; NUMBER OF SEQUENCES: 61
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 218 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein PCT-US94-14106-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 104; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US94-14106-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                        64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                      1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLOKPGOSPKLLIHKVSNRF
                                                                                                     5 DIVWTQSPLSLPVTPGEPASISCRSSQSLVHSNGDTYLHWYLQKPGQSPQLLIYKVSNRP
                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 DVVMTQTPLSLPVSPGDQASISCRSSQSLVHSYGNTYLHMYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                  65 SGVPDRFSGSGSGTDFTLKISRVEAEDVGVYXCSQSTHV-PYTFGQGTKVEIK 116
                                                                                                                                                               61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHV-PWTFGGGTKLEIK 131
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hackett, Jr., John R.
APPLICANT: Hackett, Jr., John R.
APPLICANT: Ostrow, David H.
APPLICANT: Ostrow, David H.
TITLE OF INVENTION: CONTROLS
NUMBER OF SQUENCES: 70
CORRESPENDENCE ADDRESS:
ADDRESSE: Abbott Laboratories
STREET: 100 Abbott Park Road
STREET: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 89.2%; Score 530.5; DB 3; Length 131; Best Local Similarity 91.2%; Pred. No. 3.4e-44; Matches 103; Conservative 4; Mismatches 5; Indels 1
                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,939
  88.5%; Pred. No. 3e-44;
tive 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl I.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5865.US.01
TELECOMMUNICATION INFORMATION:
TELEFRONS: 847-938-1729
TELEFAX: 847-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-09-070-637-20
; Sequence 20, Application US/09070637A
; Patent No. 6132722
                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08589939
Patent No. 6015662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 amino acids
Best Local Similarity 88.5
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                      US-08-589-939-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-589-939-7
                                                                      ठ
                                                                                                               g
                                                                                                                                                               ઠ
                                                                                                                                                                                                      유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

Gaps

1;

Length 638;

61 SGVPDRFSGSGGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113 RESULT 14 US-08-398-613A-48

```
1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SGVPDRFSGSGSGTDFTLRISRVEAEDLGLYFCSQSTHV-PLTFGAGTKLELK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 88.0%; Score 523.5; DB 1; Length 131; Best Local Similarity 90.3%; Pred. No. 1.6e-43; Matches 102; Conservative 6; Mismatches 4; Indels 1
                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/ms-LOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,612A
FILING DATE: 01-MaR-1995
CLASSIFICATION: 424.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398611
FILING DATE: 01-Mar-1995
APPLICATION NUMBER: 08/205864
FILING DATE: 01-Mar-1995
ATORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B. 659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
REGISTRATION NUMBER: 34,659
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SECONDAIL SECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           completed: April 18, 2005, 10:07:35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 131 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: Linear
US-08-398-612A-48
                                                                    94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                        APPLICANT: FONG, Sherman
APPLICANT: FONG, Sherman
APPLICANT: Hobert, Caroline Alice
APPLICANT: Leong, Steven R.
TITLE OF INTEWRION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory
NUMBER OF SEQUENCES: 58
CORRESPONDENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEBE: Generecch, Inc.
STREET: AGO Point San Bruno Blvd
CITY: South San Francisco
CONTRY: Outh San Francisco
CONTRY: Outh San Francisco
CONTRY: Outh San Francisco
COMPUTER INBW Compatible
COMPUTER INBW Compatible
COMPUTER INBW Compatible
CORPUTER INBW COMPATION:
APPLICATION NUMBER: US/08/398,613A
FILING DATE: 01-MAR-1994
ATTORNEY/AGRIT INPORMATION:
APPLICATION NUMBER: 08/20564
ATTORNEY/AGRIT NUMBER: 08/20564
ATTORNEY/AGRIT NUMBER: 08/20564
ATTORNEY/AGRIT NUMBER: 08/20564
TELERAN: 415/225-489
TELERAN: 415/225-489
TELERAN: 415/225-489
TELERAN: 11NFORMATION FOR SEQ ID NO: 5800ENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DVVMTQTPLSLPVTPGEPASISCRSSQSLVHRNGNTYLHWYLQKPGQSPKLLIHKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DIVMTQTPLSLPVSLGDQASISCRSSQSLVHGIGNTYLHWYLQKPGQSPKLLIYKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/08398612A
| Patent No. 5686070
| GENERAL INFORMATION:
| APPLICANT: Docerbuk, Claire M. APPLICANT: Docerbuk, Claire M. APPLICANT: Tong, Sherman
| APPLICANT: Kim, Kyung Jin | APPLICANT: Leong, Steven R. TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for TITLE OF INVENTION: Treatment of Inflammatory Disorders NUMBER OF SEQUENCES: 58
| CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc. ADDRESSEE: Genentech, Inc. Street 460 Point San Bruno Blvd CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.6e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.0%; Score 523.5; 90.3%; Pred. No. 1.6
Sequence 48, Application US/08398613A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 90.33
Matches 102; Conservative
                              Patent No. 5677426
GENERAL INFORMATION:
APPLICANT: Fong, 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-398-613A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-398-612A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

Gaps

This Page Blank (uspto)

```
RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP42957
                                                                                                                                          (without alignments)
704.902 Million cell updates/sec
                                                                                                                                                                                               US-10-737-208A-2
593
1 EVQLVQSGAEVEKFGASVKI.......YYCVSGMEYWGQGTSVTVSS 113
                                                                                                                   April 18, 2005, 09:41:10 ; Search time 62 Seconds
                                                                                                                                                                                                                                                                                                                                                                                    2105692
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                            2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003s:*
geneseqp2003bs:*
geneseqp2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A_Geneseq_16Dec04:*
                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
                                                                                                                     Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Adp42957 Humanised Adp42961 Humanised Aae27853 Mouse 14. Adg67525 14.18 ant Adg67527 14.18 ant Mouse 14. 14.18 ant Murine mo Mouse 14. 14.18 ant Mouse 14. 14.18 ant Mouse 14. 14.18 ant Mouse 14. 14.18 ant Mouse sin Binding d Synthetic 14. ant 14. ant Amino aci Mouse vir U7.6 heav 14.18 Mouse 14.18 Mouse Description Aar11597 N Adac77851 N Adac77841 N Adg67781 Adg67781 Adg67781 Adg67521 Adg6751 Adg1742 SUMMARIES ADP42957 ADP42961 ADP42961 ADG67525 AAE27855 AAE27855 AAE27851 ADG67523 AAE27851 ADG67523 ADG6753 ADG6753 ADG6753 AAE27843 AABG67515 AAB27847 ADG67519 AAE27845 ADG67517 ADD25452 ADM42727 ADM42727 ADM42727 ADM42727 ADM42727 ADM42727 8 Query Match Length 1000.0 1000.0 944.6 944.6 943.8 993.8 990.4 990.4 888.9 888.9 888.4 888.4 888.7 97.9 493.5 493.5 493.5 479.5 473.5 Score Result Š. しまくまり 14.18

Aar88752 scFv U7.6 Adj57084 3G4 antib Adj57088 3G4-2BVH- Aar88754 scFv U7.6 Aaw90226 Anti-87.2 Aaw90217 Bispecifi Aau70768 Hepatitis AdC85022 HBV HBCAG AdK14579 Hepatitis AdK85022 Anti-87.1 Aaw90227 Anti-87.1 Aaw90227 Anti-87.1 Aaw90228 Anti-87.1 Aaw9028 Anti-87.1 Aaw90218 Bispecifi Aab09776 TWV 30K m Adr73598 Humanised Adr73598 Humanised Adr73598 Humanised Adr73598 Humanised	
AAR88752 ADJ57084 ADJ57088 AAR867088 AAR86722 AAW90222 AAW90217 AAW90227 AAW90227 AAW90223 AAW90223 AAW90223 AAW90218 AAR9623 AAR9644579	ABP96756 ABP96755 AAW84097
11252 8 8 11252 8 8 22623 2 2266 8 2 2266 8 2 2266 8 2 2266 8 2 2266 8 2 2266 8 2 2266 8 3 3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	14 6 17 2
00000000000000000000000000000000000000	76. 76.
44444444444444444444444444444444444444	452.5 452.5 452
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	444

ശ
H
-
~
œ
=
€
z
ťή
\sim
Н
~

Ź

ADP42957 standard; protein; 113

ADP42957;

immunoglobulin; variable region; antibody; GD2; cytostatic; gene therapy; cancer; cell surface glycosphingolipid. New modified m14.18 antibodies with reduced immunogenicity and that specifically bind the human cell surface glycosphingolipid GD2, useful for treating cancer. Humanised immunoglobulin heavy chain variable region SEQ ID NO:2. 67...98
/label= huVHFR3
/note= "framework region 3"
/130...130...13
/label= huVHFR4
/note= "framework region 4" /note= "framework region 1" 'note= "framework region 2" Claim 2; SEQ ID NO 2; 51pp; English cocation/Qualifiers 1. .25 /label= huVHFR1 36. .49 /label= huVHFR2 16-DEC-2003; 2003WO-EP014295 17-DEC-2002; 2002US-0433945P (MERE) MERCK PATENT GMBH WPI; 2004-488049/46. Gillies SD, Lo K; WO2004055056-A1 23-SEP-2004 01-JUL-2004 Synthetic. Key Region Region Region Region

Best Local Similarity

a

```
The invention relates to a novel antibody variable region, where the antibody variable region specifically binds to human cell surface glycosphingolipid GD2. An antibody variable region of the invention has cytostatic activity, and may have a use in gene therapy. The antibody may be used for treating cancer. The nucleic acid or cell is useful for manufacturing a medicament that may be used for treating diseases such as cancer. The present sequence represents humanised immunoglobulin heavy chain variable region.
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel antibody variable region, where the antibody variable region specifically binds to human cell surface glycosphingolipid GD2. An antibody variable region of the invention has cytostatic activity, and may have a use in gene therapy. The antibody may be used for treating cancer. The nucleic acid or cell is useful for manufacturing a medicament that may be used for treating diseases such as cancer. The present sequence represents an immunoglobulin heavy chain-IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulin, variable region; antibody; GD2; cytostatic; gene therapy; cancer; cell surface glycosphingolipid; IL-2.
                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        m14.18 antibodies with reduced immunogenicity and that bind the human cell surface glycosphingolipid GD2, useful
                                                                                                                                                                                                                                                                                     EVQLVQSGAEVEKPGASVXISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                           1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanised immunoglobulin heavy chain-IL-2 fusion protein SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                             113
                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                        NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS
                                                                                                                                                                                               Length 113;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                  Score 593; DB 8; Pred. No. 2e-45;
                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 6; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP42961 standard; protein; 575
                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-DEC-2002; 2002US-0433945P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-DEC-2003; 2003WO-EP014295
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MERE ) MERCK PATENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-488049/46.
N-PSDB; ADP42959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New modified m14.18
                                                                                                                                                                                                           Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion protein.
                                                                                                                                                             Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004055056-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specifically
for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gillies SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                          19
                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP42961;
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        ADP4296:
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                      g
```

Length

DB 8;

100.0%; Score 593;

Sequence 575 AA;

Query Match

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  derived from a parent fusion protein, comprising first and second proteins/polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is non-immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in combining known favourable properties of a composition or in creating new properties of a composition which elicits biological or pharmacological efficacy without having undesirable physiological effects such as nausea or gastric upset. The present sequence is mouse 14.18 antibody modified epitope. This sequence is used in the exemplification of the invention
                                                          9
                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                          Mouse; fusion protein; immunological; major histocompatability complex; MHC; gastric upset; nausea; 14.18 antibody.
                                                        1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                      EVOLVOSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVOLVQSGAEVEKPGASVKISCKASGSSFTGYNMWWRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an immunogenically modified fusion protein
                                                                                                                                     61 NQKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVIVSS 113
                                                                                                                    61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New modified fusion protein with reduced immunogenicity, usefu combining favorable properties of a composition, comprises an immunoglobulin molecule linked to a non-immunoglobulin target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 113;
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hamilton A,
                               ö
            Pred. No. 1.1e-44; 
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 561; DB 5;
Pred. No. 1.5e-42;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ຜັ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carter G,
Way JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 19; Page 78; 92pp; English.
                                                                                                                                                                                                                            Æ
                                                                                                                                                                                                                                                                                                                 Mouse 14.18 antibody VH region #1.
100.08; F1.
                                                                                                                                                                                                                         AAE27853 standard; protein; 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones T,
Baker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.6%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-FEB-2002; 2002WO-EP001690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-2001; 2001EP-00103955.
05-APR-2001; 2001EP-00108291.
                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 94.7
Matches 107; Conservative
                             113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carr FJ,
Watkins J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-667054/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       WO200266514-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide.
                                                                                                                                                                                                                                                                                     13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-AUG-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gillies S,
                                                                                                                                                                                                                                                        AAE27853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanlon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
                          Matches
                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                       g
                                                                                                                    ઠે
                                                                                                                                             g
                                                          ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS
                                                       RESULT 5
                                                                                                 유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (MHC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically nonmodified biological molecule identified is useful for preparing a modified biological extivity, where the T-cell epitope desired biological activity, where the T-cell epitope is a limer peptide. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                   human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 94.6%; Score 561; DB 5; Length 113; Best Local Similarity 94.7%; Pred. No. 1.5e-42; Matches 107; Conservative 2; Mismatches 4; Indels
                                                                                                                              14.18 antibody VH mouse peptide threaded modified epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                              Hamilton A;
                                                                                                                                                                                                                                                                                                                                                                                                                             Williams S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 21; Page 66; 85pp; English.
                                                              ADG67525 standard; protein; 113
                                                                                                                                                                                                                                                                                                                                                                                                                              Jones T,
                                                                                                                                                                                                                                                                                                                    2001EP-00106899.
2001EP-00107012.
2001EP-00107568.
                                                                                                                                                                                                                                                                                                                                                   2001EP-00110220.
2001EP-00113228.
                                                                                                                                                                                                                                                                                    2001EP-00105777
2001EP-00106536
                                                                                                                                                                                                                                                                                                                                                                         2001EP-00124965
2001EP-00126859
                                                                                                                                                                                                                                                                                                        2001EP-00106538
                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to MHC molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                             Carter G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-750424/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 113 AA;
                                                                                                                                                                                                         WO200269232-A2
                                                                                                                                                                                                                                                                                                                  20-MAR-2001;
20-MAR-2001;
27-MAR-2001;
                                                                                                                                                                                                                                                                         19-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                   25-APR-2001;
30-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-2001;
                                                                                                                                                                                                                                                   18-FEB-2002;
                                                                                                                                                                                                                                                                                   08-MAR-2001;
15-MAR-2001;
                                                                                                                                                                                                                                                                                                        15-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                         19-OCT-2001;
                                                                                                          11-MAR-2004
                                                                                                                                                                                                                             06-SEP-2002
                                                                                    ADG67525;
            61
                                                                                                                                                                                                                                                                                                                                                                                                                             Carr FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding
           음
```

```
derived from a parent fusion protein, comprising first and second proteins, Polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is non-immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in combining known favourable properties of a composition or in creating new properties of a composition or in creating new properties of a composition which elicits biological or pharmacological effects such as nausea or gastric upset. The present sequence is mouse 14.18 antibody modified epitope. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                    Mouse, fusion protein, immunological, major histocompatability complex; MHC; gastric upset, nausea; 14.18 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVOLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVQLLQSGPELEKPSASVMISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New modified fusion protein with reduced immunogenicity, useful for combining favorable properties of a composition, comprises an immunoglobulin molecule linked to a non-immunoglobulin target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an immunogenically modified fusion protein
                       113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMBYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Williams
61 NOKFKGRATLTVDKSSTAYMHLKSLTSEDTAVYYCVSGMEYWGOGTTVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOKFKGRATLTVDKSSSTAYMHLKSLTSEDSAVYYCVSGMEYWGQGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%; Score 556; DB 5; Length 113; 92.9%; Pred. No. 4.1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamilton A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ο̈
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carter G,
Way JC;
                                                                                                                                                                 Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 19; Page 78; 92pp; English.
                                                                                                                                                                                                                                                                                                                             Mouse 14.18 antibody VH region #2.
                                                                                                                                                              AAE27855 standard; protein; 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones T,
Baker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-FEB-2001; 2001EP-00103955. 05-APR-2001; 2001EP-00108291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-2002; 2002WO-EP001690
                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERE ) MERCK PATENT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr FJ,
Watkins J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-667054/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200266514-A2.
                                                                                                                                                                                                                                                                         13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gillies S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanlon M,
                                                                                                                                                                                                                     AAE27855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG67527
ID ADG6
```

ö

ADG67527 standard; protein; 113 AA.

9 9

g ò

chimaeric binding protein; immunoglobulin; variable region; mouse.

1. .19 /label= leader peptide

20. .118 /label= variable

20. .153

119. .132 /label= J(H4)

Jocation/Qualifiers

fus musculus

Peptide Protein Region Region Region

řey

133. .153 /label= constant region

89US-00409889 89US-00409889

20-SEP-1989; 20-SEP-1989;

WO9104329-A. 04-APR-1991, (ABBO) ABBOTT LAB

Gillies SD;

Murine monoclonal 14.18 H chain V region.

(first entry)

14-JUN-1991

standard; protein; 153 AA.

AAR11597 AAR11597;

```
The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (WHC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful tor preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically non-modified biological molecule with reduced immunogenicity and having a retained desired biological activity, where the T-cell epitope is a limer peptide. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                     human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide binding to MHC molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hamilton A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%; Score 556; DB 5; 92.9%; Pred. No. 4.1e-42; ive 4; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams S,
                                                                                                          14.18 antibody VH mouse modified epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 21; Page 67; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001EP-00107568.
2001EP-00110220.
2001EP-00113228.
2001EP-00124965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones T,
                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-2002; 2002WO-EP001688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001EP-00106536
2001EP-00106538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001EP-00106899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001EP-00107012
                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 93.8
Best Local Similarity 92.9
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carter G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-750424/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 113 AA;
                                                                                                                                                                                                                                                                                                         WO200269232-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-2001;
20-MAR-2001;
27-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-2001;
15-MAR-2001;
15-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-NOV-2001;
                                                        11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                    16-SEP-2002
ADG67527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carr FJ,
                                                                                                                                                                                                                                                       Mus sp.
```

```
Two separate H and L chain cDNA libraries were prepared from mRNA isolated from the murine hybridoma cell line 14.18. The lambda gt10 library was enriched for full-length L- and H-chains. It was screened by filter hybridisation using various C region probes. The phage clones from each screening were analysed further by restriction analysis. The longest H cDNA sequence was sequenced. It appears to encode a normal length Igleader peptide. To ensure translation starts from the second ATG codon once additional 5' sequences have been added to the insert, the cDNA is truncated by limited Bal31 exonuclease treatment. An XhoI linker was then added to give a sequence which, when expressed, will result in an mRNA encoding a normal Ig leader sequence and a functional variable region. The deduced amino acid sequence is given here. See also AAQ11292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 EVOLLOSGPELEKPSASVMISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein prodn. - e.g. having dual biological activity, esp. antibodies, by transfecting host cell with constructed cassette and second DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NOKFKGRATLITVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 556; DB 2;
Pred. No. 5.7e-42;
4; Mismatches 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example, Fig 2; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 92.9
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1991-117518/16.
N-PSDB; AAQ11291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

ö

Gaps

.; 0

4; Indels

1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY

9 9

113

NOKFKGRATLTVDKSTSTAYMILKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS

19 61

g ò

ð

RESULT 7

```
Jones T,
                                                                                                                                                                                15-MAR-2001; 2001EP-00106538
20-MAR-2001; 2001EP-00106899
20-MAR-2001; 2001EP-00107012
                                                                                                                                                                                                                   27-MAR-2001, 2001EP-00107568
25-APR-2001, 2001EP-00110220,
30-MAY-2001, 2001EP-00113228,
19-OCT-2001, 2001EP-00124965,
12-NOV-2001, 2001EP-00126859,
                                                                                                                      18-FEB-2002; 2002WO-EP001688
                                                                                                                                                                     2001EP-00106536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                            (MERE ) MERCK PATENT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                       binding to MHC molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                    Carr FJ, Carter G,
                                                                                                                                                                                                                                                                                                                                            WPI; 2002-750424/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 113 AA;
                                                                      WO200269232-A2
                                               Unidentified
                                                                                                                                                                     15-MAR-2001;
                                                                                              06-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE27841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an immunogenically modified fusion protein derived from a parent fusion protein, comprising first and second proteins/polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is non-immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in combining known favourable properties of a composition or in creating new properties of a composition which elicits biological or pharmacological or pastric upset. The present sequence is mouse 14.18 antibody modified epitope. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                     Mouse; fusion protein; immunological; major histocompatability complex; MHC; gastric upset; nausea; 14.18 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVQLLQSGPELKKPGASVKISCKASGSSFTGYNMNWVRQAIGQRLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                        Williams S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New modified fusion protein with reduced immunogenicity, useful combining favorable properties of a composition, comprises an immunoglobulin molecule linked to a non-immunoglobulin target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                Mouse 14.18 antibody de-immunised VH5 modified epitope.
                                                                                                                                                                                                                                                                                                        Hamilton A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.4%; Score 536; DB 5; Le
Best Local Similarity 88.5%; Pred. No. 2.5e-40;
Matches 100; Conservative 7; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.18 antibody de-immunised VH5 modified epitope.
                                                                                                                                                                                                                                                                                                       Carter G,
Way JC;
        AAE27851 standard; protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ź
                                                                                                                                                                                                                                                                                                                                                                                                                               Example 19; Page 78; 92pp; English
                                                                                                                                                                                                                                                                                                       Jones T, (
Baker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG67523 standard; protein; 113
                                                                                                                                                                                                                                            19-FEB-2001; 2001EP-00103955.
05-APR-2001; 2001EP-00108291.
                                                                                                                                                                                                                   18-FEB-2002; 2002WO-EP001690
                                                                                                                                                                                                                                                                               (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                       Carr FJ,
Watkins J,
                                                                                                                                                                                                                                                                                                                                            WPI; 2002-667054/71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 113 AA;
                                                                                                                                                                     WO200266514-A2.
                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide.
                                                         13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-2004
                                                                                                                                                                                            29-AUG-2002
                                                                                                                                                                                                                                                                                                      Gillies S,
                                                                                                                                                                                                                                                                                                                     Hanlon M,
                                 AAE27851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG67523;
                                                                                                                                            Мив вр.
                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BXHXXX
```

```
The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (MHC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful for preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically non-modified biological molecule identified is useful for preparing a biological activity, where the T-cell epitope is a limer peptide. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide
human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOKFKGRATLITVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.4%; Score 536; DB 5; Length 11
88.5%; Pred. No. 2.5e-40;
ive 7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamilton A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williams S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 21; Page 66; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE27841 standard; protein; 113 AA
```

Mus

ø

```
The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (HMC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful for preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically non-modified biological molecule identified is useful for preparing a biological molecule with reduced immunogenicity and having a retained desired biological activity, where the T-cell epitope is a lamer peptide. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLLQSGPELKKPGASVKISCKASGSSFTGYNMNWVRQAPGQRLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide binding to MHC molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.9%; Score 527; DB 5; Length 113; llarity 87.6%; Pred. No. 1.6e-39; Conservative 8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 21; Page 65; 85pp; English.
                                                                                                                                                     08-MAR-2001; 2001EP-00105777.
15-MAR-2001; 2001EP-00106536.
15-MAR-2001; 2001EP-00106638.
20-MAR-2001; 2001EP-00106899.
20-MAR-2001; 2001EP-00107012.
27-MAR-2001; 2001EP-00107568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones T,
                                                                                   18-FEB-2002; 2002WO-EP001688
                                                                                                                                                                                                                                                                                                                  30-MAY-2001; 2001EP-00113228.
                                                                                                                                                                                                                                                                                                                                                                   12-NOV-2001; 2001EP-00126859
                                                                                                                                                                                                                                                                                                                                                                                                               (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carr FJ, Carter G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-750424/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
tes 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE27849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    datches
              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an immunogenically modified fusion protein derived from a parent fusion protein, comprising first and second proteins/polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is non-immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in properties of a composition or in creating new properties of a composition which elicits biological or pharmacological efficacy without having undesirable physiological effects such as nause efficacy without having undesirable physiological effects such as nause or gastric upset. The present sequence is mouse 14.18 antibody modified epitope. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                            Mouse; fusion protein; immunological; major histocompatability complex; MHC; gastric upset; nausea; 14.18 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New modified fusion protein with reduced immunogenicity, useful for combining favorable properties of a composition, comprises an immunoglobulin molecule linked to a non-immunoglobulin target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NQKFKGRATLSVDKSSSQAYMFLKSLTSEDSAVYYCVSGMEYWGQGTTVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                           Hamilton A, Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.9%; Score 527; DB 5; Length II.
87.6%; Pred. No. 1.6e-39;
Migmatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.18 antibody VH veneered modified epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                           Carter G,
Way JC;
Mouse 14.18 antibody VH modified epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 19; Page 77; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADG67513 standard, protein, 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         Jones T,
Baker M,
                                                                                                                                                                                                                                                                                                   19-FEB-2001; 2001EP-00103955.
05-APR-2001; 2001EP-00108291.
                                                                                                                                                                                                                                                       18-FEB-2002; 2002WO-EP001690
                                                                                                                                                                                                                                                                                                                                                                        (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.57
Best Local Similarity 87.65
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Carr FJ,
Watkins J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-667054/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 113 AA;
                                                                                                                                                            WO200266514-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide.
                                                                                                                                                                                                           29-AUG-2002
```

Hamilton A;

Williams S,

Gillies S, Hanlon M,

```
Mouse; fusion protein; immunological; major histocompatability complex; MHC; gastric upset; nausea; 14.18 antibody.
NQKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
            Mouse 14.18 antibody de-immunised VH4 modified epitope.
                                                                                 ¥.
                                                                              AAE27849 standard; protein; 113
                                                                                                                                                                                                          Mus sp
```

WO200269232-A2

Unidentified

11-MAR-2004

ADG67513;

61

유 ò g

ö

Gaps

ö

Indels

Hamilton A;

Williams S,

```
The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (HGC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful for preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically non-modified biological molecule with reduced immunogenicity and having a retained desired biological activity, where the T-cell epitope is a lamer peptide. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; fusion protein; immunological; major histocompatability complex; MHC; gastric upset; nausea; 14.18 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLLQSGPELKKPGASVKISCKASGSSFTGYNMNWVRQAPGQRTEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                              Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide binding to MHC molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse 14.18 antibody de-immunised VH1 modified epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.7%; Sco. No. 3c. 86.7%; Pred. No. 3c. 7; Mismatches
                                                                                                                                                                                                                                                                                                                                               Example 21; Page 66; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE27843 standard; protein; 113 AA
               15-MAR-2001; 2001EP-00106538.

20-MAR-2001; 2001EP-00106699.

27-MAR-2001; 2001EP-00107012.

27-MAR-2001; 2001EP-00107568.

25-ARR-2001; 2001EP-00110220.

30-MAR-2001; 2001EP-0011328.

19-CTT-2001; 2001EP-00134965.
                                                                                                                                                                                                  Jones T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-2002; 2002WO-EP001690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-FEB-2001; 2001EP-00103955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                (MERE ) MERCK PATENT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98; Conservative
                                                                                                                                                                                                Carr FJ, Carter G,
                                                                                                                                                                                                                               WPI; 2002-750424/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200266514-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE27843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Мив вр.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an immunogenically modified fusion protein derived from a parent fusion protein, comprising first and second proteins/polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is non-immunoglobulin target polypeptide each linked to the other directly or by a linker combining known famourable properties of a composition or in creating new properties of a composition which elicits biological or pharmacological properties of a composition which elicits biological effects such as nauses or gastric upset. The present sequence is mouse 14.18 antibody modified epitope. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMWWRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVOLLOSGPELKKPGASVKISCKASGSSFTGYNMNWVRQAPGORTEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
                                                                                                                                                                                 ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQKFKGRVTITVDKSSSQAYMHLKSLTSEDTAVYYCVSGMEYWGQGTTVTVSS 113
                                                                                                                                                                                 Hamilton A, Williams
                                                                                                                                                                                                                                                          New modified fusion protein with reduced immunogenicity, useful combining favorable properties of a composition, comprises an immunoglobulin molecule linked to a non-immunoglobulin target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.4%; Score 524; DB 5; Length 113;
86.7%; Pred. No. 3e-39;
tive 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.18 antibody de-immunised VH4 modified epitope.
                                                                                                                                                                               Carter G,
Way JC;
                                                                                                                                                                                                                                                                                                                                              Example 19; Page 78; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG67521 standard; protein; 113 AA
                                                                                                                                                                               Jones T,
Baker M,
                                                                18-FEB-2002; 2002WO-EP001690
                                                                                             19-FEB-2001; 2001EP-00103955.
05-APR-2001; 2001EP-00108291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-2001; 2001EP-00103954
08-MAR-2001; 2001EP-00105777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-2002; 2002WO-EP001688
                                                                                                                                             (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                             Carr FJ,
Watkins J,
                                                                                                                                                                                                                               WPI; 2002-667054/71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 113 AA;
WO200266514-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200269232-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-2002
                                                                                                                                                                             Gillies S,
                                                                                                                                                                                              Hanlon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG67521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

ö

Gaps

; 0

5; Length 113; 8; Indels

Score 524; DB 5, Pred. No. 3e-39;

```
ô
                                                                                                                                                                                                                                                  derived from a parent fusion protein, comprising first and second proteins/polypeptides, where the first protein is an immunoglobulin molecule or its fragment and the second protein is non-immunoglobulin target polypeptide each linked to the other directly or by a linker molecule. The immunogenically modified fusion protein is useful in combining known favourable properties of a composition or in creating new properties of a composition which elicits biological or pharmacological efficacy without having undesirable physiological effects such as nausea or gastric upset. The present sequence is mouse 14.18 antibody modified epitope. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVQLVQSGABVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                      The invention relates to an immunogenically modified fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; mouse; T-cell epitope; major histocompatibility complex; MHC; immunogenicity; MHC class II; antibody.
                                                               Williams S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NQKFKSRVTITADKSSSQAYMHLKSLTSEDTAVYYCVSGMEYWGQGTTVTVSS 113
                                                                                                                                        useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS
                                                                                                                                                  combining favorable properties of a composition, comprises an immunoglobulin molecule linked to a non-immunoglobulin target
                                                                                                                                                                                                                                                                                                                                                                                                                                             87.9%; Score 521; DB 5; Length 113;
85.8%; Pred. No. 5.5e-39;
Live 7; Mismatches 9; Indels
                                                                                                                                 modified fusion protein with reduced immunogenicity,
                                                             Hamilton A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.18 antibody de-immunised VH1 modified epitope.
                                                               Ö
                                                             Carter G,
Way JC;
                                                                                                                                                                                                            Example 19; Page 77; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADG67515 standard; protein; 113 AA
                                                            Jones T, (Baker M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001EP-00106899.
2001EP-00107012.
2001EP-00107568.
2001EP-00110220.
05-APR-2001; 2001EP-00108291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001EP-00105777.
2001EP-00106536.
2001EP-00106538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-2002; 2002WO-EP001688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001EP-00113228
                           (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                            Carr FJ,
Watkins J,
                                                                                                       WPI; 2002-667054/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200269232-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-2001; 2
08-MAR-2001; 2
15-MAR-2001; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-2001;
30-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2002
                                                                           Hanlon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                          Gillies
                                                                                                                                   New
 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
The invention relates to a novel method for identifying one or more potential T-cell epitope peptides within the amino acid sequence of a biological molecule by determining the binding of the peptides to major histocompatibility complex (WHC) molecules using in vitro or in silico techniques or biological assays. The method of the invention is useful to preparing a polypeptide, a protein, a fusion protein, an antibody or their fragments with reduced immunogenicity. The potential T-cell epitope peptide within the amino acid sequence of a parent immunogenically non-modified biological molecule dentified is useful for preparing a modified biological molecule with where the T-cell epitope is a lamer peptide. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                   Identifying potential T-cell epitope peptides within the amino acid sequence of a biological molecule, useful for preparing a biological molecule with reduced immunogenicity, comprises determining peptide binding to MHC molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 113;
                                                                                                       Hamilton A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.9%; Score 521; DB 5;
85.8%; Pred. No. 5.5e-39;
ive 7; Mismatches 9.
                                                                                                       Williams S,
                                                                                                                                                                                                                                                                                      Example 21; Page 66; 85pp; English.
                                                                                                         Ļ
19-OCT-2001; 2001EP-00124965.
12-NOV-2001; 2001EP-00126859.
                                                                                                         Jones
                                                           (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 85.8 les 97; Conservative
                                                                                                     Carter G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 113 AA;
                                                                                                     Carr FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
  ઠે
```

Job time : 64 secs

09

NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113

61

원 경 경

```
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

April 18, 2005, 09:57:11; Search time 11.5 Seconds (without alignments) 945.434 Million cell updates/sec Run on:

Title: Perfect score:

US-10-737-208A-2 593 1 EVQLVQSGAEVEKPGASVKI.......YYCVSGMEYWGQGTSVTVSS 113 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	471.5	79.5	137	7	H32513	Iq heavy chain pre
	467.5	78.8	119	~	F30502	chain
٣	459	77.4	118	7	PL0200	ti-DNA
4	441.5	74.5	118	7	PL0084	heavy
S	440.5	74.3	150	~	PN0444	heavy chain
9	427.5	72.1	112	N	809957	Ig heavy chain V-D
7	426.5		114	7	S26319	Ig heavy chain V r
80		71.9	139	~	A27609	heavy
6	425.5	71.8	135	~	PS0057	heavy chain
10	424.5	71.6	120	~	E45722	:i-glycoprote
11	424	71.5	151	~	PL0011	heavy chain
12	423.5	71.4	118	-	MHMS38	
13	418.5	70.6	128	~	137267	heavy
14	417.5	70.4	118	~	836265	heavy
15	416	70.2	119	~	PH0099	heavy
16	414	69.8	117	-	MHMS4E	heavy chain
17	414	69.8	140	~	T01407	heavy
18	412	69.5	117	H	MHMSJS	Ig heavy chain V r
19	410.5	69.2	120	~	S41394	heavy
20	410.5	69.2	135	N	849530	anti-Sm antibody V
21	409	69.0	116	~	S55542	heavy
22	409	69.0	119	~	B53285	g heavy
23	409	69.0	125	~	PH0100	
24	409	69.0	142	7	A32483	Ig heavy chain V r
25	408.5	68.9	120	~	F45722	anti-glycoprotein
56	408	68.8	107	N	PH0971	Ig heavy chain V r
27	406.5	68.5	136	N	JL0077	Ig heavy chain pre
28	406	68.5	119	~	PH0961	heavy chain
29	406	68.5	138	~	PH0105	anti-digoxin trans

Ig heavy chain V r	Ig heavy chain v r	Ig heavy chain V r	heavy chair	Ig heavy chain V r	heavy chair	lB leader/Ic	hea	hea	Ig heavy chain V r	Ig heavy chain V-1	Ig heavy chain pre	Ig heavy chain V-1	Iq mu chain precur	Ig heavy chain V r	Ig heavy chain pre
PH0962	A49982	PH0958	PH0887	C37267	MHMS18	PC4402	PH0952	866537	PH0960	A33548	804575	C33548	S14683	PH0954	PS0024
~	~	~	~	7	-	4	~	~	~	7	~	7	~	~	N
120	120	122	122	128	139	287	128	131	136	129	140	133	627	132	139
8.4	68.2	68.2	68.2	68.0	67.9	67.9	67.7	67.7	67.7	67.6	67.6	67.5	67.5	67.4	67.4
ø		5.	4.5	3.5	02.5	02.5	01.5	01.5	101.5	401	401	400	400	399.5	99.5
	404.5	404	40	40	4	4	4	4.	•					.,	m

ALIGNMENTS

Ig heavy chain precursor V region (BXW16) - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: H32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and A;Reference number: A94689; MUD:88331394; PMID:3138286
A;Accession: H32513
A;Molecule type: DNA
A;Residues: 1-137 <KOF>
A;Crose-references: GB.M20831; NID:9196949; PIDN:AAA38848.1; PID:9196950
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology < IMM>

Gaps 5, 79.5%; Score 471.5; DB 2; Length 137; 76.3%; Pred. No. 6.3e-36; Live 11; Mismatches 12; Indels 5. Query Match Best Local Similarity 76.3% Matches 90; Conservative

ij

9 20 BIQLQQSGABLVKPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWIGNINPYYGSTSY 79 1 EVOLVOSGAEVEKPGASVKISCKASGSSFTGYNMNWVRONIGKSLEWIGAIDPYYGGTSY g ò

61 NOKEKGRATLIVDKSTSTAYMILKSLRSEDTAVYYCV----SGMEYWGQGTSVTVSS 113 80 NQKFKGKATLIVDKSSSTAYMQLNSLTSEDSAVYYCARKNYGSSFDYWGQGTTLIVSS 137 ò g

F30504C
G. Species: Mus musculus (house mouse)
C. Species: Mus musculus (house mouse)
C. Species: Mus musculus (house mouse)
C. Accession: F30502
R. Filat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A. Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mis.
A. Reference number: A30502; MUID:88315787; PMID:2457627
A. Accession: F30502
A. Status: preliminary
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Molecule type: mRNA
C. Superfamily: immunoglobulin V region; immunoglobulin homology
C. Reywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <INM>

Gaps 7; Length 119; Indels Query Match 78.8%; Score 467.5; DB 2; Best Local Similarity 74.8%; Pred. No. 1.3e-35; Matches 89; Conservative 11; Mismatches 12;

.

ï

```
Ig heavy chain V region precursor - human (fragment)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cidate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
Cidate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
Cidates Non444
Rikaluza, B: Betzl, G: Shao, H:, Diamantsein, T:; Weidle, U.H.
Rikaluza, 31-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polymera
A;Reference number: PN0444; MUID:93138402; PMID:1339379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Igiheavy chain V-D-J region (106-10E) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
C;Accession: 809957
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodie
A;Reference number: 809955; MUID:90269328; PMID:2347362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 BVQLQQFGABLVKPGTSVKISCKASGYIFTDYNMDWVKQSHGKSLEWIGDIDPNFDSSSY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
             61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVS----GMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLQQSGPELVKSGASVKMSCKASGYTFTDYYMNWVKQSHGKSLEWIGRVNPSNGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID:9930213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-150/Product: Ig heavy chain V region #status predicted <MAT>
F:20-117/Domain: variable region <VRG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: PN044
A,Molecule type: mRNA
A,Residues 1915: GKAL>
A,Residues 1915: AKAL>
A,Cross.references: GB:L02346
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
C,Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-112 < REL:
A; Residues: 1-112 < REL:
A; Cross-references: EMBL:X51845; NID:955244; PIDN:CAA36138.1; P:
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
74.3%; Score 440.5; DB 2
Best Local Similarity 72.9%; Pred. No. 4.5e-33;
Matches 86; Conservative 11; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 72.1%; Score 427.5; DB Best Local Similarity 73.5%; Pred. No. 5e-32; Matches 83; Conservative 12; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
S26319
                                                                                                    셤
                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ୍ ନ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
S;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
A;Title: Structural characterization of antidiotypic antibodies; evidence that Ab2s are
A;Reference number: PL0080; MUID:89094248; PMID:2492056
A;Residues: 1-118 *MES-
A;R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clacestion: PLO200
No. 1 May 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij.
                  9
                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGM------EYWGQGTSVT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-DNA autoantibody BV16-19, heavy chain V region - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J heavy chain V region (E4) - mouse
Species: Mus musculus (house mouse)
Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                  1 BVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 74.5%; Score 441.5; DB 2; Best Local Similarity 72.0%; Pred. No. 2.8e-33; Matches 85; Conservative 12; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.4%; Score 459; DB 2; 74.6%; Pred. No. 7.3e-35; tive 10; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;31-35/Region: complementarity-determining 1
F;50-6/Region: complementarity-determining 2
F;9-110/Region: complementarity-determining 3
F;9-106/Region: D region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 74.6*
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;107-118/Region: JH region
                                                                                                                                                                        61
                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                             g
                                                                                                                                                                    ò
                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
```

```
A; Accession: PS0057
A; Molecule type: DNA
A; Residues: 1-135 < YAO.
A; Accession: PS0057
A; Molecule type: DNA
A; Residues: 1-135 < YAO.
A; Cross-references: GB:D00307; NID:g220448; PIDN:BAA00213.1; PID:g220449
A; Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gl;
C; Comment: The gene encoding this protein was isolated from a hybridoma that produces a: C; Superfermily: immunoglobulin vegiobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 1-19/Domain: signal sequence #status predicted <SIG>F; 20-115/Product: Ig heavy chain V region PAR #status predicted <MAT>
F; 34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B45722
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasq. J. Virol. 67, 489496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on his A;Reference number: A45722; MUID:93100833; PMID:7677958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-151 <CHE>
A;Experimental source: cell line 4C11
C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 YNQKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVS-----GMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lig heavy chain precursor V region (4C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: PL0011
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
MOL. Immunol, 25, 33-40, 1988
A;Fitle: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 EVQLQQSGPELVKPGASVKISCKASGYSFTGYPMYWVKQSHGKSLEWIGRINPYNGDTFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVOLOQSGPELVKPGASMKISCKASVYSFTGYTMNWVKQSHGONLEWIGLINPYNGGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIG-AIDPYYGGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVOLVOSGAEVEKPGASVKISCKASGSSFTGYNMNWVRONIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 NQKFKGKATLTVDKSSSTAHMELRSLTSEDSAVYYCARLNYRGAYWGQGTLVTVSA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVS---GMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                         Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-120 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: sequence extracted from NCBI backbone (NCBIP:120593) C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: glycoprotein C;Keywords: glycoprotein F;15-99/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
      A; Reference number: PS0057; MUID:89197817; PMID:2467902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 424.5; DB 2;
Pred. No. 1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 425.5; DB 2; Pred. No. 9.3e-32; 10; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.6%;
70.8%;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 73.3%;
Matches 85; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: E45722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: PL0011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Johnson Chain precursor V region (129) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
C;Accession: A27609
R;Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988
A;Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain swit A;Reference number: A27609; MulD:88154467; PMID:3126234
A;Molecule type: DNA
A;Residues: 1-139 <a href="https://document.com/district/">https://document.com/district/</a>
A;Cross-references: EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PID:g553992
C;Generics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology circle (*Superfamily: immunoglobulin v region I29 #status predicted <VAR>
F;34-117/Domain: immunoglobulin homology circle (*MM>)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: PS0057
R;Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.
J. Biochem. 104, 337-343, 1988
A;Title: Biased expression of variable region gene families of the immunoglobulin heavy
                                                                         C. Accession: $26319
R. Stark S. E. ; Caton, A.J.
D. Exp. Med. 114, 613-624, 1991
A. Title: Antibodies that are specific for a single amino acid interchange in a protein A. Reference number: $26309; MUID:91341421; PMID:1908510
A. Reference number: $26319
A. Reference number: $26319
A. Residues: 1-114 <STA>
A. Residues: 1-114 <STA>
A. Residues: inmunoglobulin V region; immunoglobulin homology
C; Reywords: heterotetramer; immunoglobulin
F;11-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS0057
Ig heavy chain precursor V region (PAR) - mouse
C;Species: Mus musculus (house mouse)
C;Species: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
                   C;Species: Mus musculus (house mouse)
C;Species: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSGPELVKPGASVKISCKASGYSFTGYFMWWVKQSHGKSLEWIGRINPYNGDTFYNQKFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVQLQQSGPELVKPGASVKMSCKASGYTFTDYVMHWVKQSNGKSLEWIGYINPYNDYTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVS-----GMEYWGQGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OSGAEVEKPGASVKISCKASGSSFTGYNMWWRONIGKSLEWIGAIDPYYGGTSYNOKFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRATLTVDKSTSTAYMHLKSLRSEDTAVYYC----VSGMEYWGQGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.9%; Score 426.5; DB 2; 70.8%; Pred. No. 7.8e-32; ive 11; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 426.5; DB 2
Pred. No. 6.3e-32;
9; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 11; Mismatches
heavy chain V region - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.9%;
ilarity 74.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 85, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠ
```

(fr.

mouse

7

Gaps

59 9

Ä

Gaps

```
C;Keywords: heterotetramer; immunoglobulin F;19-102/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.2%;
                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          VSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: PH0099
                                                                                                                                                                                                                                                                                                                                                                                                          111
                                                                                                                                                                                                                                                                                                                                                                                                                                                          126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                     원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Accession: A02040

R. P. Bovens, J.; Siekevitz, M.; Beyreuther, K.; Rajewsky, K.

EMBO J. 3, 517-523, 1984

A, Title: A V region determinant (idiotope) expressed at high frequency in B lymphocytes

A, Reference number: A91000; MUID:84182519; PMID:6201362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody properties of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEY----WGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVS----GMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J heavy chain V region (AC38 205.12) - mouse
Species: Mus musculus (house mouse)
Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 heavy chain V region (129) - mouse C, Species: Mus musculus (house mouse)
C, Species: Mus musculus (house mouse)
C, Species: Mus musculus (house mouse)
C, Species: Musculus (house mouse)
C, Accession: 137267
R, Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A, Fitle: Heavy and light chain variable region sequences and antibody proper A, Reference number: A38740; MUID: 91177923; PMID: 1706720
A, Accession: 137267
A, Status: preliminary; not compared with conceptual translation
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-128 < RUF>
C, Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                    20 BVQLQQSGPBLLKPGASVKISCKASGYTFTDYTMHWVKQSHGKSLEWIGGFDPNYDNTFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMWWKQSHGKSLEWIGDINPNNGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Superfamily: immunoglobulin immunoglobulin is signal sequence #status predicted <SIG>F;1-19/Domain: signal sequence #status predicted <SIG>F;20-136/Product: IG heavy chain V region 4C11 #status predicted <MAT>F;34-117/Domain: immunoglobulin homology <IPM>F;34-117/Domain: immunoglobulin homology <IPM>F;34-117/Domain: omplementarity-determining 1 F;69-88/Region: complementarity-determining 2 F;118-125/Region: complementarity-determining 3 F;118-125/Region: complementarity-determining 3 F;137-151/Domain: C region (fragment) #status predicted <COR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 118;
                                                                                                                                                                                                                                                                    71.5%; Score 424; DB 2; Length 151; 70.1%; Pred. No. 1.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A/Accession: A02040
A/Molecule type: protein
A/Residues: 1-118 <DIL.2
A/Cross-references: UNIPROT: P06330
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.4%; Score 423.5; DB 1
Best Local Similarity 71.2%; Pred. No. 1.2e-31;
Matches 84; Conservative 10; Mismatches 19
                                                                                                                                                                                                                                                                                                                    13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;105-118/Rēgion: J sēgment
F;22-96/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99-104/Region: D segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-98/Region: V segment
                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                       82;
                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
Ig heavy chain V region (anti-cyclosporin F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000
C;Accesion: PH0099
R;Schmitter, D; Poch, O; Zeder, G; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; V.A.) Iungunol. 27, 1029-1038, 1990
A;Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
A;Reference number: PH0087; MUID:91042649; PMID:2122240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S36265
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. BMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries. A;Reference number: S36256; MUID:93178448; PMID:7679990
                                                                                                                                                                                                                                                                                                                                       66 QKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCARRGITTVVAKSYYFDYWGQGTTLT 125
                                                                                                                                                         61
                                                                                                                                                                                                                               65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDFLSGYLDYWGQGTLVTVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Homo sapiens (man)
C.Date: 03-Peb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
                                                                                                                                                                                            6 VQLQQSGPELVKPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGGINPNNGGTSYN
                                                                                                                                                                                                                                                                                            62 OKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSG-------MEYWGQGTSVT
                                                                                                                                              2 VQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVOLVOSGAEVEKPGASVKISCKASGSSFTGYNMAWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1118 <GRI>
A;Residues: 1518 <GRI>
A;Cross-references: EMBL:Z18846; NID:G33121; FIDN:CAA79298.1; PID:g939900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NOKFKGRATLIVDKSTSTAYMILKSLRSEDTAVYYC----VSG-MEYWGQGTSVTVSS
                                                                         Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
           Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-119 <SCH>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; E>98 Domain: immunoglobulin homology <IMM>
F; B>98 Domain: immunoglobulin homology <IMM>
F; B>98 Domain: immunoglobulin homology <IMM>
F; B>98 Domain: immunoglobulin homology <IMM>
F; B>96 Region: complementarity-determining 1
F; C=66 Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C:Species: Homo saniens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 70.4%; Score 417.5; DB 2; Local Similarity 70.3%; Pred. No. 4.3e-31; nes 83; Conservative 14; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA
; Score 418.5; DB ; Pred. No. 3.8e-31 13; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F,99-106/Region: complementarity-determining 3
   70.6%;
                                                                     82; Conservative
```

Score 416;

```
Best Local Similarity 70.1%; Pred. No. 5.9e-31;
Matches 82; Conservative 13; Mismatches 18; Indels 4; Gaps 1;
                        ò
                                        qq
                                                        ઠે
```

Search completed: April 18, 2005, 10:06:47 Job time: 12.5 secs

g

This Page Blank (uspto)

musculu musculu

musculu

musculu musculu

mus mus mus mue

musculu musculu

0924p5 0924p9 0924p9 0924f2 0924r7 096pjb2 0914a2 0914a2 0924p6 0924p6

musculu musculu

mus .

musculu

```
61 NQKFKGKATLIVDKSSSTAYMQLKSLTSEDSAVYYCAVIYYGNSPAWFAYWGQGTLVTVS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLQQSGPELEKPGASVKISCKASGYSFTGYNANAVKQSNGKSLEWIGNIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCV-----SGMEYWGQGTSVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307935; AAL09420.1; -.
HSSP; P01751; INQB.
SMART; SM0406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON TER 120 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.4%; Score 477; DB 2; Length 120; larity 77.5%; Pred. No. 2.2e-41; Conservative 7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Pterin-mimicking anti-idiotope heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 120
120 AA; 13204 MW; DC4834ABIDE56F3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                 120 AA
                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                              Q924P6
HV11 MOUSE
Q96QS0
                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
             Q924P5
Q924P9
Q8K0F2
                                                         092405
0924R7
09DBL4
06PJB2
092402
091VA2
                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-DNA heavy chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 19, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] -
SEQUENCE FROM N.A.
STRAIN=C3H/HeJ-lpr/lpr;
 (Fragment).
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                            01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=J558;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                 Q920E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBVIJ1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                 RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mus musculu .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mus musculu
mus musculu
mus musculu
mus musculu
mus musculu
mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o sapien
musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mus musculu
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         schistosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculu
                                                                                                                      (without alignments)
684.792 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mus r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mus
                                                                                                                                                                                           EVQLVQSGAEVEKPGASVKI......vycvsgmeywgqgtsvtvss
                                                                                                   April 18, 2005, 09:42:15 ; Search time 84.5 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3920e8
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                    1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBVIJ1
Q9QXE9
HV51 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HV12_MOUSE
098K172
092K172
0924Q9
0924Q9
0924R1
0924R1
0924R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HV07 MOUSE
Q924Q7
Q924R5
Q924Q4
Q924Q8
                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2652R6
                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2920E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27TMK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q91WR1
                                                                                                                                                                                                                                                                                                                                                                                                                              UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                           US-10-737-208A-2
593
1 EVQLVOSGAEVEKPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145
145
145
146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \begin{array}{c} 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\ 177 \\
                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435
423.5
423.5
423.5
412.5
415.6
412.5
412.5
411.5
411.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411
409
409
408
407.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               405.5
403.5
403.5
403.5
402.5
400.5
400.5
                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                  Total number
                                                                        OM protein
                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
```

112

9

Gaps

NON TER NON TER SEQUENCE

Query Match

Matches

ò 유 ò 셤 ò g

```
1 EVOLVOSGAEVEKPGASVKISCKASGSSFIGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEY-----WGQGTSVTVSS 113
                                                                                                                                                                                                                              Diddrop R., Bovens J., Sievettz M., Beyreuther K., Rajewsky K.;
Diddrop R., Bovens J., Sievettz M., Beyreuther K., Rajewsky K.;
A V region determinant (idiotope) expressed at high frequency in B lymphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523[194].
EMBO J. 3:517-523[194].
ENROS P. PO1751; INQB.
InterPro; IPRO710; Ig-like.
InterPro; IPRO710; Ig-like.
Fram: PPF0047; ig-v.
Fram: PPF0047; ig-v.
SWART; SW00406; igv.
SWART; SW00406; igv.
Usect protein sequencing; Immunoglobulin V region.

V segment.
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.4%; Score 423.5; DB 1; Length 118; 71.2%; Pred. No. 7.18-36; ive 10; Mismatches 19; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clemens A., Rademaekers A., Specht C., Koelsch E., Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AJC32171; CAB65236.1; -.
PIR; PH0973; PH0973; PH0973; PH0973; INOB.
InterPro; IPR07110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IRR003596; Ig-v.
SMART; SM0406; IGV; 1.
PROSITE; PSC0835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 118
118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 117
117 AA; 13060 MW; D816AD0858A47E4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Immunoglobulin heavy chain V-D-J region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.3%; Score 423; DB 2; 70.9%; Pred. No. 8e-36;
                         01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
19 heavy chain V region AC38 205.12.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              V segment.
D segment.
J segment.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                            SEQUENCE.
MEDLINE=84182519; PubMed=6201362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9QXF0
Q9QXF0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSG------MEYWGQGTSVT 110
                                                                                                                                                                                                                                                                                                                                                                                                                    Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S., "Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from CJH-lpyr mice and lupus mice with nephritis.";

Bur. J. Immunol. 26:2225-233(1996).

EMBL, V195149, AAB02916.1;

SWART; SM00406; IGV;

PROSTIT: PS50815; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                      1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVS----GMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 BVQLQQSGPELVKPGASVKASCKASGYTFTDYYMKAVKQSHGKSLEWIGDINPNNGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                             73.5%; Score 436; DB 2; Length 123;
68.3%; Pred. No. 3.8e-37;
tive 11; Mismatches 18; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemens A., Rademaekers A., Specht C., Koelsch E., Clemens A., Rademaekers A., Specht C., Koelsch E., Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AJ225.74; CAB65237.1; -...
FIR; F33932; F33932.
HISSP, P01751; INO.
InterPro; IPR00110; Ig-like.
InterPro; IPR003596; Ig-v.
PROSTIT: SM04406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Indels
                                                                                                                                                                                        123 123
123 AA; 13806 MW; CC0037AB06E9911E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Immunoglobulin heavy chain V-D-J region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.4%; Score 435; DB 2; 73.5%; Pred. No. 4.6e-37; ive 10; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
MEDLINE=96409289; PubMed=8814271;
                                                                                                                                                                                                                                                               Local Similarity 68.3%
les 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 73.5%,
Matches 86, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 VSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
HV51_MOUSE
ID _HV51_MOUSE
```

090XE9

엄 ò

ઠ

RESULT 3 Q9QXE9

Gaps

5,

Length 117;

Matches

ઠે 셤 ò g

265ZR6; Q652R6

```
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Haich F.,
Diatchenko.L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S.M., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Annara M.A., Marra M.A.,
Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCV----SG----MEYWGQGTSVTVS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 NQKFKGKATLIYUDKSSSTAYMELNSLISEDSAVYYCARYYYSGSYWYFDVWGAGTTVTVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 EVQLQQSGPELVKPGASVKISCKASGYTFTGYYMHWVKQSHGKSLEWIGLVNPSNGDTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRONIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE-Kidney;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.2%; Score 416; DB 2; Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC055910; AAH55910.1;
HSSP; P01865; 1KB5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.4%; Pred. No. 2e-3 ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CZECH II; TISSUE-Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR00306; Ig_MRC.
InterPro; IPR003596; Ig_v.
Pfam; PR07654; Cl-8et; 3.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Igh-VJ558 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 $ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Igh-VJ558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q91WR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q91WR1
         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1,
                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             τwο
                                                                                                                                      61 NOKFKGRATLIVDKSISTAYMHLKSLRSEDTAVYYCVSG----MEYWGQGISVTVSS 113
                                                                                                                                                                61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSG----MEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                           1 EVÓLOGSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rueff-Juy D., Marche P.N., Drapier A.-M., Cazenave P.-A.;
"Junctional diversity of H and L chains allows the coexpression of wutually exclusive idiotopes (Idilo4 and IdiS58).";
J. Immunol. 146:4024-4030(1991).
EMBL: M74139, AAA7776.1;
InterPro; IPR003599; Ig.
InterPro; IPR00110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CZECH II; TISSUB=Mammary tumor; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2004 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypochetical protein A1324046.
Name=A1324046;
Name=A1324046;
Muse musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
         4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Ab 126.33 heavy chain variable and joining regions (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 134;
    18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ### PF0047; 19; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON TER 1 1 1
SEQÜENCE 134 AA; 14908 MW; 1852D86D26FC7567 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 71.3%; Score 423; DB 2; Best Local Similarity 70.9%; Pred. No. 9.3e-36; Matches 83; Conservative 12; Mismatches 18
    12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 AA
                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91237115; PubMed=1709665;
                                                                                                                                                                                                                                                                                                                                             25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
  83; Conservative
                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78
```

O7TMK1;

Q7TMK1

RESULT 7

g ò a

8

9 79

Gaps

```
Q8K172
                     ઠે
                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                               g
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodiigues S., Sanchez A.,
RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Moriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marram M.A.;
T and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGM------EYWGQGTSV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 NOKFKGKATLIVDKSSSIAYMQLNNLISDDSAVYYCARGPVYYSYFSYDRGDYWGQGTLV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 EVQLQQSGPELVKPGASVKLSCKASGYTITDYYVNWVKQSHGKSLEWIGDINPYNGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
19 heavy chain V region MOPC 104E.

Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, AND CARBOHYDRATE-LINKAGE SILE OLL SEQUENCE, MEDLINE=83075344; PubMed=6816276; MEDLINE=83075344; PubMed=6816276; Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H., Hood L.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013339, AAH1339.1; -.
HSSP; P01751; 1A6W.
MGD; MGI:96486; Igh-VJ558.
MGD; MGI:96486; Igh-VJ558.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IGV; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SEQUENCE 488 AA; 52964 MW; F12068460B9D CRC64;
                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.1%; Score 415.5; DB 2; 65.3%; Pred. No. 2.3e-34; Wismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 65.3%; Pred. No. 2...
Watches 81; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 AA
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 TVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 TVSA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HV12 MOUSE
P01756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HV12_MOUSE
               용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
Chromer's From N.N.

MEDINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REALINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Wolfey K.M., Sodergen B.J., Lu X., Gibbs R.A.,

Richards S., Wolfey K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Tageneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                               61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDYDWYFDVWGAGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                             61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEY----WGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                      1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                   Glycoprotein; Immunoglobulin V region.
                                                                                                                                                                                                                                                                               4
                                                                                                                      ig-like.
By similarity.
N-linked (GlcNAc. . .) (complex)
                                                                                                                                                                                                                                      Length 117;
                                                                                                                                                                                                                                                                             19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=mix FVB/N; TISSUE=Mammary tumor;
Strausberg R.;
Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                        1 116 ig-like.
22 96 By similarity.
55 55 N'linked (GlcNAC. . .) (cc
117 117 AA, 12983 MW, 3CF8ACE4BE447E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                        Score 414; DB 1;
Pred. No. 6.8e-35;
                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
InterPro; IPR007110; 1g-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSTIE; PS50835; IG LIKE; 1.
Direct protein sequencing; Glyco
                                                                                                                                                                                                                                      69.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                Ouery Match
Best Local Similarity 70.17,
Best Local Similarity
Best Local Similarity
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, BC028249; AAH28249.1;
PIR, F33932; F33932.
PIR, PH1105;
PIR, PH1108; PH1108.
PIR; PH1114; PH1114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Igh-VJ558 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Igh-VJ558
                                                                                                                                      DISULFID
                                                                                                                                                                           NON TER
SEQUENCE
```

us-10-737-208a-2.rup

```
61 NOKFKGRATLITVDKSTSTAYMHLKSLRSEDTAVYYCVS----GMBYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                           61 NQKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSG----MEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=80078170; PubMed=6765983; Schilling J., Clevinger B., Davie J.M., Hood L.; "Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements in heavy chain V-region gene segments.";
                                                                                                                                                                                                                                      ŝ
                                                                                                                                                                                                         69.6%; Score 412.5; DB 2; Length 143; 67.8%; Pred. No. 1.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.5%; Score 412; DB 1; Length 117; 70.1%; Pred. No. 1.1e-34;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                              143 AA; 15868 MW; 139B2E966B81E07F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13024 MW; 292E2AF4BE447E41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
19 heavy chain V region J558.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig-like.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
                                                                                                                                                                                                                                      12; Mismatches
                              PIR; PH1149; PH1149.
PIR; PH1150; PH1150.
PIR; PH1151; PH1151.
PIR; PH1152; PH1152.
PIR; PH1153; PH1153.
PIR; PH1153; PH1153.
HSSP; PO1751; 1A6W.
SMART; SMO406; IGY; 1.
                                                                                                                                                                                                                       Best Local Similarity 67.89
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                 HV13 MOUSE
P01757;
                                                                                                                                                                NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
    2222222222222Ff8
                                                                                                                                                                                                                                                                                               요
                                                                                                                                                                                                                                                                                                                                                                                                                                  요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                20 QVQLQQPGABLVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGKKY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NQKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCV----SGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                     5.
                                                                                                                                                                                                                                                                                                                                                                       Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6;
Kozono Y., Kozono H., Azuma T.;
Submitted (40G-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067790; BAB63275.1; -.
                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; Cl-set; Z.
SMART; SM00406; IGV; I.
PROSITE; PS00835; IG_LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SRQUENCE 482 AA; $\overline{5}2121 MW; A0\overline{6}F0835771D084 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q924R0;
01-DBC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                     ch 69.7%; Score 413.5; DB 2; 1 Similarity 67.8%; Pred. No. 3.7e-34; 80; Conservative 12; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                             PH1151.
PH1152.
PH1153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F33932.
PH1105.
PH1108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PH1114.
PH1118.
PH1119.
                                                                                                   PH1139.
PH1142.
PH1149.
PH1150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                          PH1131.
PH1134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PH1125.
PH1126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PH1128.
PH1129.
                                                           PH1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F28833; F28833
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
PIR; PH1118;
PIR; PH1119;
PIR; PH1125;
PIR; PH1128;
PIR; PH1131;
PIR; PH1131;
PIR; PH1139;
PIR; PH1149;
PIR; PH1149;
PIR; PH1150;
PIR; PH1150;
PIR; PH1151;
                                                                                                                                                  PH1150;
                                                                                                                                                                PH1151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PH1114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PH1142;
```

Q924R0

RESULT 11 Q924R0

PERS, PERS,

Query Match

윱

ઠે

us-10-737-208a-2.rup

RESULT 13

셤

092406

```
1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWYRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NOKFKGRATLITVDKSTSTAYMHLKSLRSEDTAVYYCVS-----GMEYWGQGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 145;
                                                                                                                Kozono Y., Kozono H., Azuma T.,
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067791; BAB63276.1; -.
PIR; F28833; F28833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CS7BL/6;
Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 AA; 16001 MW; 0F409EB09FA333D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0924R1;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VH186.2-D-J-C mu protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 69.4%; Score 411.5; DB 2;
Local Similarity 66.7%; Pred. No. 1.6e-34;
les 80; Conservative 12; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145 AA
         VH186.2-D-J-C mu protein (Fragment).
Name=VH186.2-D-J-C mu;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                        SEQUENCE FROM N.A.
STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                               PIR; PH1153; PF
HSSP; P01751; 1
SMART; SM00406;
                                                                                                                                                               F33932; I
                                                                                                                                                                                                                         PH1119;
                                                                                                                                                                                                                                                                                                                                                       PH1147;
PH1149;
PH1150;
PH1151;
PH1152;
                                                                                                                                                                                                                                                          PH1128;
                                                                                                                                                                                                                                                                                                                    PH1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                            PIR;
PIR;
PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0924R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                             PIR;
PIR;
PIR;
PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVS-----GMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                    Mus musculus (Mouse).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.4%; Score 411.5; DB 2; Length 145; 66.7%; Pred. No. 1.6e-34; live 12; Mismatches 21; Indels 7;
                                                                                                                                                                                                                                        Kozono Y., Kozono H., Azuma T.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB067794; BAB63279.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145
16011 MW; 9BC0846D40DF97EA CRC64;
                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                            Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 AA
                                                                          145
                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-OCT-2003 (TrEMBLrel. 25, Last and
WH186.2-D-J-C mu protein (Fragment).
Name=VH186.2-D-J-C mu;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 66.7%
les 80; Conservative
                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                      F33932.
PH1105.
PH1108.
PH1114.
                                                                                                                                                                                                                                                                         PIR; F28833; F28833.
PIR; F33932; F33932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 AA;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6;
                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PH1142; EPH1144; EPH1147; E
                                                                                                                                                                                                                                                                                                  PH1105;
PH1108;
                                                                                                                                                                                                                                                                                                                                                                       PH1126;
PH1128;
PH1129;
                                                                                                                                                                                                                                                                                                                                               PH1119;
PH1125;
                                                                                                                                                                                                                                                                                                                        PH1114;
                                                                                                                                                                                                                                                                                                                                     PH1118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PH1149;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PH1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                       092406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
```

Best Loc Matches

셤 ò

à

RESULT 14 Q924Q9 ID Q924Q AC Q924Q DT 01-DE DT 01-OC

ä

Gaps

7;

9 9

v

EMBL; AB067789; BAB63274.1;

```
1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69.4%; Score 411.5; DB 2; Length 145; Best Local Similarity 66.7%; Pred. No. 1.6e-34; Matches 80; Conservative 12; Mismatches 21; Indels 7,
R PIR; F33932; F3393.

R PIR; F33932; F3393.

R PIR; P33932; F3393.

R PIR; P31105; PH1106.

R PIR; PH1105; PH1108.

R PIR; PH1119; PH1119.

R PIR; PH1126; PH1126.

R PIR; PH1129; PH1128.

R PIR; PH1139; PH1139.

R PIR; PH1131; PH1131.

R PIR; PH1137; PH1131.

R PIR; PH1144; PH1137.

R PIR; PH1147; PH1144.

R PIR; PH1151; PH1144.

R PIR; PH1151; PH1151.

R PIR; PH1152; PH1153.

R PIR; PH1153; PH1153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

Search completed: April 18, 2005, 10:03:56 Job time : 85.5 secs

À

```
(without alignments)
536.541 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-737-208A-2
593
1 EVQLVQSGAEVEKFGASVKI......YYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.ppp:*
| CGn2_6/ptodata/1/pubpaa/US10B_PUBC
                                                                                                                                                                                                                                          April 18, 2005, 10:04:06 ; Search time 70 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1421835 segs, 332370683 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0.
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                                                                                                        Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			,	686, App	17, Ap	8, App	2019, Ap	4, App	15, Ap	4, App	05, Ap	2, App	13, Ap	6, App	07, Ap	
			Description	Sequence 68	Sequence 20:				Sequence 20:		Sequence 200					
SUMMARIES			1D	US-10-468-370-686	US-10-468-496-2017	US-10-468-370-688	US-10-468-496-2019	US-10-468-370-684	US-10-468-496-2015	US-10-468-370-674	US-10-468-496-2005	US-10-468-370-682	US-10-468-496-2013	US-10-468-370-676	US-10-468-496-2007	
		1	an :	15	16	15	16	15	16	15	16	15	16	15	16	
		Query	rengru	113	113	113	113	113	113	113	113	113	113	113	113	
	dю	Query	March	94.6	94.6	93.8	93.8	90.4	90.4	88.9	88.9	88.4	88.4	87.9	87.9	
			score	561	561	556	556	536	536	527	527	524	524	521	521	
		Result		7	7	٣	4	Ŋ	9	7	œ	6	10	11	12	

TYPE: PRT
CAGANISM: Artificial Sequence
FEATURE:
COMMER INFORMATION: MHC class II binding epitope
US-10-468-370-686

14	520	87.7	113	16	US-10-468-496-2011		
15	5 T 2	7.08	113	۲ <u>۲</u>	US-10-468-3/0-6/8		
17	າຕ	n	259	1 4	US-10-207-655-13		
18	493.5	83.2	259	14	US-10-053-530-13	Sequence	13, Appl
19	73	0 0	152	16	US-10-642-120-2		
2 2 2 3 3	3.5	0	152	19	US-10-642-122-2		
22	73	σ	152	16	US-10-642-124-2		
53	73	0 0	152	9 .	US-10-621-269-2		
2 6	. E	ת ס	152	9 4	US-10-620-850-2 US-10-642-116-2		
26	2.5	n on	152	11	US-10-642-100-2		
27	73	6	152		US-10-642-058-2		
28	73	σ,	152		US-10-642-121-2	Sequence	
29	464	σ (130		US-09-839-447A-3	m	
30	464	200	130	4 1	US-10-153-271-3	Sequence	<u> </u>
32	404	o u	1120		02-10-363-060A-3	Seguence	_ ~
3 6		o u	771		02-03-03-03-03-03-03-03-03-03-03-03-03-03-	משתישישים אי	
3.6	452	v	117		US-10-223-880-5	Sequence	
35	451.5	ဖ	118		US-10-462-062-139	Sequence	
36	21	9	118		US-10-462-062-140	Sequence 1	٠.
37	21	9	137		US-10-462-062-153	Sequence	-:
38	21	9	137		US-10-462-062-154	Sequence	-:
39	450.5	9	120		US-10-372-719-2	Sequence	٠
40	4	s o	261		US-10-689-006-24	Sequence	2.
41	5.	S)	116		US-10-389-155-16	Sequence	
24.	ഗ	S C	116		US-10-389-417-16	Sequence	~ :
4. 4 E 4.3	δ.	s) L	116		US-10-452-357-57	Seguence	
4. 4 4. 1.	445		116	1 5	US-09-215-163-44 TR-10-763-424-50	Seguence	
2	,	?	244		00-121-00-01-00	ליכווכה	י אם
					ALIGNMENTS		
RESULT 1							
US-10-468	8-370-6	86					
; Sequen	ce 686,	Applica	tion U	1,0	468370		
	ation No.	Publication No. US20040	4008203	39A1			
; GENERA	L INFOR	DRMATION:	•				
; APPLI		illies,	Stephen	_			
; APPLICANT:		Carr, Francis J.	ancie				
; APPLI		Jones, 1	mr.				
; APPLI		Carter,	Graham				
, APPLI		Hamiltor	ı, Anita				
; APPLI		Williame	s, Stepr	en			
; APPLI		Hanlon,	Marian				
, APPLICANT:		Watkins,	B, John				
, APPLI	CANT:	Baker, P	lactnew feren				
; APPLI	CANT	way, Jei	rey	4 4 7	debilded limits owner, or		
TITLE OF I	OF IN	TITE OF INVENTION: AKILFICIAL F	TAMETA	12	INVENTION: ARITICIAL FROIDING WITH REDUCED		
	PEFFF	CE. MER-	118	į	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		
CIRRE	NT APPI.	TCATION	NIMBER	113	/10/468.370		
	NT FILI	NG DATE:	2003	-08-			
	APPLIC	ATION NO	MBER: F	EP 011	1103955.9		
	FILING	DATE: 2	2001-02	-19			
PRIO	APPLIC	R APPLICATION NUMBER: 1	MBER: 1	Q,	01108291.4		
PRIO	FILING	DATE: 2	001-04	-05			
	APF	ATION NO	5	۲ کار:	PCT/EP02/01690		
, PRIOR	7 6	DATE	Σ.	81.			
SOFTWARE C	į	AT SEO FOR	r Windows	3	Version 4.0		
SEO ID	•	7			•		
·吕		113					
. HOVE	ä						

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            පු
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         심
                                                                                                                                                                                                                                                                                                                                                                        KESULT 2

US-10-468-496-2017

Sequence 2017, Application US/10468496

Publication No. US2040180186A1

GENERAL INFORMATION:

APPLICANT: Carter, Graham

APPLICANT: Carter, Graham

APPLICANT: Williams, Stephen

TITLE OF INVENTION: IMMUNOSER: US/10/468,496

CURRENT FILING DATE: 2001-02-19

PRIOR PELING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-15

PRIOR PLING DATE: 2001-03-15

PRIOR PLING DATE: 2001-03-15

PRIOR PLING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 2036

SOFTWARE: RESERVE FOR Windows Version 4.0

SEQ ID NO 2017

LENGTH: 113
                                                             ö
                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                               1 EVQLVQSGPEVEKPSASVKISCKASGSSFTGYNMNWVRQAIGKSLEWIGAIDPYYGGTSY
                                                                                                            1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNNNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLVQSGPEVEKPSASVKISCKASGSSFTGYNMNWVRQAIGKSLEWIGAIDPYYGGTSY
                                                          0; Gaps
                                                                                                                                                                                                                                                         61 NQKFKGRATLITVDKSSSTAYMHLKSLTSEDTAVYYCVSGMEYWGQGTTVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NOKFKGRATLTVDKSSSTAYMHLKSLTSEDTAVYYCVSGMEYWGQGTTVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 94.6%; Score 561; DB 16; Length 113; Best Local Similarity 94.7%; Pred. No. 3.2e-44; Matches 107; Conservative 2; Mismatches 4; Indels
Query Match
94.6%; Score 561; DB 15; Length 113;
Best Local Similarity 94.7%; Pred. No. 3.2e-44;
Matches 107; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: MHC class II binding epitope US-10-468-496-2017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                    원
                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                              à
```

US-10-468-370-688

Sequence 688, Application US/10468370
Fublication No. US20040082039A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Garr, Francis J.
APPLICANT: Garr, Francis J.
APPLICANT: Carre, Graham
APPLICANT: Carter, Graham

```
APPLICANT: JOHN AND ADDRESS, 11M
APPLICANT: Hamilton, Anita
APPLICANT: Hamilton, Anita
APPLICANT: Hamilton, Anita
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: IMMUNOGENCITY
FILE REPERBENCE: MER-117
CURRENT APPLICATION NUMBER: 0103954.2
FRICA FILING DATE: 2001-02-19
FRICA FILING DATE: 2001-02-19
FRICA FILING DATE: 2001-03-08
FRICA FILING DATE: 2001-03-08
FRICA FILING DATE: 2001-03-08
FRICA FILING DATE: 2001-03-08
FRICA FILING DATE: 2001-03-15
FRICA FILING DATE: 2001-03-15
FRICA FILING DATE: 2001-03-15
FRICA FILING DATE: 2001-03-15
FRICA FILING DATE: 2001-03-20
FRICA RELING DATE: 2001-03-20
FRICA FILING DATE: 2001-03-20
FRICA FRICA FILING DATE: 2001-03-20
FRICA FILING DATE: 2001-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NOKFKGRATLITVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NOKFKGRATILTVDKSSSTAYMHLKSLTSEDSAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 556; DB 15; Length 113;
Pred. No. 9.2e-44;
4; Mismatches 4; Indels
APPLICANT: Markins, John
APPLICANT: Watkins, John
APPLICANT: Watkins, John
APPLICANT: Baker, Matthew
APPLICANT: Baker, Matthew
APPLICANT: Watkins, John
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
TITLE OF INVENTION: IMMUNGENICITY
FILE REPERENCE: MEL-18
CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT APPLICATION NUMBER: EP 01103955.9
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR FILING DATE: 2001-02-19
PRIOR FILING DATE: 2002-02-18
RIOR RELING DATE: 2002-02-18
NUMBER OF SEQ ID NOS: 689
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 688
LENGHH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2019, Application US/10468496
Publication No. US20040180386A1
GENERAL INFORMATION:
APPLICANT: Carter, Graham
APPLICANT: Jones, Tim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 92.9%;
Matches 105; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus Musculus
US-10-468-370-688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-468-496-2019
```

```
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      요
                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                      1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                       1 EVQLLQSGPELEKPSASVMISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVQLLQSGPELKKPGASVKISCKASGSSFTGYNWNWVRQAIGQRLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                             NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                        61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                         .
0
                                                                                Query Match
93.8%; Score 556; DB 16; Length 113;
Best Local Similarity 92.9%; Pred. No. 9.2e-44;
Matches 105; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: De-immunized MHC class II binding epitope US-10-468-370-684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURTHAND IN COMPATION:

JAPPLICANT: Garr, Francis J.

APPLICANT: Garr, Francis J.

APPLICANT: Garre, Francis J.

APPLICANT: Garter, Graham

APPLICANT: Garter, Garham

APPLICANT: Hamilton, Anita

APPLICANT: Hamilton, Martian

APPLICANT: Hanis, John

APPLICANT: Way, John

TITLE OF INVENTION: IMMUNGER: US/10/468,370

CURRENT FILING DATE: 2001-08-19

PRIOR PTLING DATE: 2001-08-19

PRIOR APPLICATION NUMBER: EP 01108291.4

PRIOR APPLICATION NUMBER: PCT/EP02/01690

PRIOR APPLICATION NUMBER: 2001-04-05

PRIOR APPLICATION NUMBER: 2001-04-05

PRIOR APPLICATION NUMBER: 2001-02-18

NUMBER OF SEQ ID NOS: 689

SEQ ID NO 684

LENGTH. 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

90.4%; Score 536; DB 15;
Best Local Similarity 88.5%; Pred. No. 6.4e-42;
Matches 100; Conservative 7; Mismatches 6;
; OTHER INFORMATION: MHC class II binding epitope US-10-468-496-2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-10-468-496-2015
US-10-468-496-2015
Sequence 2015, Application US/10468496
Publication No. US20040180386A1
GENERAL INFORMATION:
APPLICANT: Carter, Francis J.
APPLICANT: Carter, Graham
APPLICANT: Jones, Tim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 684, Application US/10468370
Publication No. US20040082039A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                      8
                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                             ઠ
                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
```

```
APPLICANT MATERIAN MATERIAN CONTRIBUTION OF T-CELL
TITLE OF INVESTICAL MATERIAN MATE
```

US20040082039A1

```
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Carter, Graham
APPLICANT: Carter, Graham
APPLICANT: Carter, Graham
APPLICANT: Jones, Tim
APPLICANT: Jones, Tim
APPLICANT: Jones, Tim
APPLICANT: Hamilton, Anita
TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
TITLE OF INVENTION: IMMUNOGENCITY
FILE REFERENCE: MER-117
CURRENT APPLICATION NUMBER: 01103954.2
PRIOR PAPLICATION NUMBER: 01103954.2
PRIOR PAPLICATION NUMBER: 01105777.5
PRIOR PAPLICATION NUMBER: 01105777.5
PRIOR APPLICATION NUMBER: 0110538.0
PRIOR PLING DATE: 2001-03-15
PRIOR PLING DATE: 2001-03-15
PRIOR PLING DATE: 2001-03-15
PRIOR PLING DATE: 2001-03-15
PRIOR PLING DATE: 2001-03-20
PRIOR FILING DATE: 2001-03-20
PRIOR FILING DATE: 2001-03-20
PRIOR PLING DATE: 2001-03-20
PRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLLQSGPELKKPGASVKISCKASGSSFTGYNMNWVRQAPGQRLEWIGAIDPYYGGTSY 60
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NOKFKGRATLIVDKSISTAYMHLKSLRSEDTAVYYCVSGMEYWGQGISVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NQKFKGRATLSVDKSSSQAYMHLKSLTSEDSAVYYCVSGMEYWGQGTTVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NQKFKGRATLSVDKSSSQAYMHLKSLTSEDSAVYYCVSGMEYWGQGTTVTVSS 113
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 113;
                                                                                                                                                                                      Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

88.9%; Score 527; DB 16;
Best Local Similarity 87.6%; Pred. No. 4.3e-41;
Matches 99; Conservative 8; Mismatches 6;
                                                                                                                                                                                  Query Match

88.9%; Score 527; DB 15;
Best Local Similarity 87.6%; Pred. No. 4.3e-41;
Matches 99; Conservative 8; Mismatches 6;
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: MHC class II binding epitope US-10-468-496-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2005, Application US/10468496 Publication No. US20040180386A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-10-468-370-682
; Sequence 682, Application US/10468370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-468-496-2005
                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

```
APPLICANT: Carter, Graham
APPLICANT: Jones, Tim
APPLICANT: Hamilton, Anita
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: IMMUNGENCITY
FILE REFERENCE: MER-117
CURRENT APPLICATION NUMBER: 0110394.2
FILE REPERING DATE: 2001-02-19
FRIOR APPLICATION NUMBER: 01105777.5
FRIOR PILING DATE: 2001-03-16
FRIOR PILING DATE: 2001-03-16
FRIOR PILING DATE: 2001-03-15
FRIOR PILING DATE: 2001-03-15
FRIOR PILING DATE: 2001-03-15
FRIOR PILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVOLLOSGPELKKPGASVKISCKASGSSFTGYNMWWVRQAPGQRTEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOKFKGRVTITVDKSSSQAYMHLKSLTSEDTAVYYCVSGMEYWGQGTTVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THER INFORMATION: De-immunized MHC class II binding epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                            APPLICANT: MAIKINS, JOHN
APPLICANT: Baker, Matchew
APPLICANT: Way, John
APPLICANT: Way, Joffrey,
APPLICANT: Way, Joeffrey,
TITLE OF INVENTION: ARTHFICIAL PROTEINS WITH REDUCED
TITLE OF INVENTION: IMMUNOGENICITY
FILE REPERENCE: MRR-118
CURRENT APPLICATION UNMERR: US/10/468,370
CURRENT FILING DATE: 2003-08-19
PRIOR FILING DATE: 2001-02-19
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR PLING DATE: 2001-04-05
PRIOR PELING DATE: 2002-04-05
PRIOR FILING DATE: 2002-02-18
NUMBER OF SEQ ID NOS: 689
SOFTWARE: FASTERE for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 88.4%; Score 524; DB 15;
Best Local Similarity 86.7%; Pred. No. 8.2e-41;
Matches 98; Conservative 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2013, Application US/10468496
Publication No. US20040180386A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                    Hamilton, Anita
Williams, Stephen
Carr, Francis J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Carr, Francis J.
                              Jones, Tim
Carter, Graham
                                                                                                                                          Hanlon, Marian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-468-496-2013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-468-370-682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
```

```
Sequence 2007, Application US/10468496
Publication No. US20040180386A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carr, Francis J.
                                                                                                                 APPLICANT: Carr, Francis J. APPLICANT: Carter, Graham APPLICANT: Jones, Tim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamilton, Anita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanlon, Marian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           윱
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVQLLQSGPELKKPGASVKISCKASGSSFTGYNMNWVRQAIGQRLEWIGLIDPYYGGTSY 60
                                                                                                                                                                                                                                                                                                                                                     1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                1 EVQLLQSGPELKKPGASVKISCKASGSSFTGYNMWWYRQAPGQRTEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NQKFKGRVTITVDKSSSQAYMHLKSLTSEDTAVYYCVSGMEYWGQGTTVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMBYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                          Query Match
88.4%; Score 524; DB 16; Length 113;
Best Local Similarity 86.7%; Pred. No. 8.2e-41;
Matches 98; Conservative 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 87.9%; Score 521; DB 15; Length 113; I Similarity 85.8%; Pred. No. 1.6e-40; 97; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: De-immunized MHC class II binding epitope
US-10-468-370-676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Matking, John
APPLICANT: Baker, Matthew
APPLICANT: Baker, Matthew
APPLICANT: Baker, Matthew
APPLICANT: Baker, Jeffrey
ITTLE OF INVENTION: IMMUNOGENICITY
FILE REPERENCE: MRE-118
CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT APPLICATION NUMBER: EP 01103955.9
PRIOR FILING DATE: 2001-02-19
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR APPLICATION NUMBER: P0109291.4
PRIOR APPLICATION NUMBER: P0109291.4
PRIOR APPLICATION NUMBER: P0109291.4
PRIOR FILING DATE: 2002-02-18
                                                                                                                                                                                      OTHER INFORMATION: MHC class II binding epitope
                      NUMBER OF SEQ ID NOS: 2036
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2013
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 689
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 676, Application US/10468370 Publication No. US20040082039A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carr, Francis J.
Jones, Tim
Carter, Graham
Hamilton, Anita
Williams, Stephen
Hanlon, Marian
                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gillies, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 97; Conserva
                                                                                                                                                                                                              US-10-468-496-2013
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
```

```
APPLICANT: Williams, Stephen
APPLICANT: Williams, Stephen
APPLICANT: Williams, Stephen
APPLICANT: Williams, Stephen
APPLICANT: Hamilton, Anita
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
TITLE OF INVENTION: EPITODES AND USE FOR PREPARING MOLECULES WITH REDUCED
TITLE OF INVENTION: INMUNOGENCITY
FILE REPERENCE: MER-11)
CURRENT APPLICATION NUMBER: US/10/468,496
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: 0110577.5
PRIOR APPLICATION NUMBER: 01106538.0
PRIOR PILING DATE: 2001-03-15
PRIOR PLILNG DATE: 2001-03-15
PRIOR PLILNG DATE: 2001-03-15
PRIOR PLILNG DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 01106536.4
PRIOR APPLICATION NUMBER: 01106536.4
PRIOR APPLICATION NUMBER: 01106536.4
PRIOR APPLICATION NUMBER: 01107012.5
PRIOR APPLICATION NUMBER: 0110693.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVQLLQSGPELKKPGASVKISCKASGSSFTGYNMNWVRQAIGQRLEWIGLIDPYYGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 BVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Watkins, John
APPLICANT: Baker, Matthew
APPLICANT: Baker, Matthew
TITLE OF INVENTION: ATTIFICIAL PROTEINS WITH REDUCED
FITLE OF INVENTION: IMMUNOGENICITY
FILE REFERENCE: MER-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

87.9%; Score 521; DB 16;
Best Local Similarity 85.8%; Pred. No. 1.6e-40;
Matches 97; Conservative 7; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT FILING DATE: 2003-08-19
PRICA APPLICATION NUMBER: EP 01103955.9
PRICH FILING DATE: 2001-02-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 2036
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 680, Application US/10468370
Publication No. US20040082039A1
PERERAL INFORMATION:
APPLICANT: Gillies, Stephen
```

```
g
               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPLICANI; HABILLON, ANIER

TITLE OF INVENTION: BETTOPES AND USE FOR PREPARING MOLECULES WITH REDUCED

TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED

FILE REFERENCE: MRR-117

CURRENT APPLICATION NUMBER: US/10/468,496

CURRENT APPLICATION NUMBER: US/10/468,496

PRIOR PILING DATE: 2003-09-25

PRIOR PILING DATE: 2001-02-19

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-08

PRIOR FILING DATE: 2001-03-15

PRIOR PELING DATE: 2001-03-15

PRIOR PELING DATE: 2001-03-15

PRIOR PELING DATE: 2001-03-15

PRIOR PELING DATE: 2001-03-20

PRIOR PELING DATE: 2001-03-20

PRIOR FILING DATE: 2001-03-3-15

PRIOR FILING DATE: 2001-03-3-15

PRIOR FILING DATE: 2001-03-15

PRIOR FILING DATE: 2001-03-15

PRIOR PRIOR FILING DATE: 2001-03-15

PRIOR FILING DATE: 2001-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVOLVOSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVQLLQSGPELKKPGASVKISCKASGSSFTGYNMWWYRQAPGQRTEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 87.7%; Score 520; DB 15; Length 113; Best Local Similarity 85.8%; Pred. No. 1.9e-40; Matches 97; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
87.7%; Score 520; DB 16; Length 113;
Best Local Similarity 85.8%; Pred. No. 1.9e-40;
Matches 97; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: De-immunized MHC class II binding epitope US-10-468-370-680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: MHC class II binding epitope US-10-468-496-2011
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: PCT/EP02/01690
PRIOR FILING DATE: 2002-02-18
NUMBER OF SEQ ID NOS: 689
SOFTWARE: PREUSEQ for Windows Version 4.0
SEQ ID NO 680
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-468-496-2011; Sequence 2011, Application US/10468496; Publication No. US20040180386A1; GENERAL INFORMATION: APPLICANT: Carter, Graham; APPLICANT: Jones, Tim; APPLICANT: Williams, Stephen; APPLICANT: Hamilton, Anita
                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLLQSGPELKKPGASVKISCKASGSSFTGYNMNWVRQAPGQRTEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                             61 NQKFKGRVTITADKSSSQAYMHLKSLTSEDTAVYYCVSGMEYWGQGTTVTVSS 113
61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NQKFKSRVTITADKSSSQAYMHLKSLTSEDTAVYYCVSGMEYWGQGTTVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: De-immunized MHC class II binding epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hanlon, Marian
APPLICANT: Watkins, John
APPLICANT: Baker, Matthew
APPLICANT: Way, Jeffrey
APPLICANT: Way, Jeffrey
TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 514; DB 15;
Pred. No. 6.9e-40;
7; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/468,370
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: EP 01103955.9
PRIOR FILING DATE: 2001-02-19
PRIOR APPLICATION NUMBER: EP 01108291.4
PRIOR PILING DATE: 2001-04-05
PRIOR PELING DATE: 2002-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 689
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: April 18, 2005, 10:17:26
Job time : 70 secs
                                                                                                                                                                            Sequence 678, Application US/10468370
Publication No. US20040082039A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.0%;
Matches 96; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                              Hamilton, Anita
Williams, Stephen
                                                                                                                                                                                                                                                                                     Carr, Francis J
                                                                                                                                                                                                                                                                                                                                     Carter, Graham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: MER-118
                                                                                                                           RESULT 15
US-10-468-370-678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-468-370-678
```

102,

```
1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                         Sequence
Sequence
Sequence
                                                                                                                                                                          Sequence
Sequence
Sequence
              Sequence
                                                                                                                  Sequence
Sequence
Sequence
                                                                                                                                                   Sequence
                                     Sequence
                                                Sequence
                                                                                                        Sequence
                                                                                             Sequence
                                                                                                                                                                                                                                                                                     .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,324
FILING DATE: 19930108
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/COMPUTION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
US-08-436-717-102
US-09-581-345-5
US-08-561-521-41
US-08-561-521-41
US-08-881-037-20
US-08-137-117D-112
US-08-436-717-112
US-08-436-717-728-56
US-08-477-078-56
US-08-474-040-56
US-08-487-200-56
US-08-487-200-56
US-08-487-200-56
US-08-487-200-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 473.5; DB 2
; Pred. No. 2.6e-40;
13; Mismatches 10
                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 981-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-002-324-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                               ≨
                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MU
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90;
                                                                                                                                                                                                                                                                   RESULT 1
US-08-002-324-2
                                                         Query Match
Best Local S:
Matches 90
    임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 30, Appli
Sequence 78, Appli
Sequence 63, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8, Appli
8, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appl
Appl
Appl
Appl
Appl
Appl
Appl
                                                                                             (without alignments)
443.965 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 63, Ap
Sequence 139, A
Sequence 140, A
Sequence 153, A
Sequence 2, App
Sequence 2, App
Sequence 55, App
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
                                                                                                                           US-10-737-208A-2
593
1 EVQLVQSGAEVEKPGASVKI......YYCVSGMEYWGQGTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                April 18, 2005, 09:57:36; Search time 19 Seconds
                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-419-788-30

US-08-55-539A-78

US-08-625-539A-63

US-09-647-468-139

US-09-647-468-153

US-09-647-468-153

US-09-647-468-154

US-09-647-468-154

US-09-647-468-154

US-09-647-68-154

US-09-58-156-8

US-08-177-728-57

US-08-477-728-57

US-08-477-728-57

US-08-477-728-57

US-08-477-728-57

US-08-477-728-57

US-08-477-728-57

US-08-474-040-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-137-117D-27
US-08-137-117D-102
US-08-436-717-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-487-200-57
US-08-487-200-57
US-08-487-200-73
US-08-484-50
                                                                                                                                                                                                                               Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -08-484-537-57
-08-484-537-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-002-324-2
                                                                                                                                                                                                           513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          protein search, using sw model
                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                         Issued Patents AA:*
                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133
133
116
116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473.5
473.5
                                                                                                                                                                          Scoring table:
                                                                                                                                         Perfect score:
                                                          OM protein
                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                        Database
                                                                                Run on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.
```

9

Gaps

i,

Gaps

4;

Length 130;

```
1 IQLQQSGAELVKPGASVKISCKASGYSFTGYNMNWVKQSHGKSLEWIGNINPYYGSTSYN 60
                                                                                                                                                                                                            2 VOLVOSGABVEKPGASVKISCKASGSSFIGYNMNWVRQNIGKSLEWIGAIDPYYGGTSYN
                                                                                                                                                                                                                                                                                                                     61 QKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARGKGTGFAYWGQGTLVTVSA 116
                                                                                                                                                                                                                                                                                             62 OKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCV----SGMEYWGQGTSVTVSS 113
                                                                                                                    Query Match
78.2%; Score 464; DB 4; Length 13
Best Local Similarity 76.7%; Pred. No. 2.6e-39;
Matches 89; Conservative 10; Mismatches 13; Indels
             ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Oligonucleotide
US-09-556-605-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NQKFKGKATLIVDKSSSTAYMQLSSLTSEDSAVYFCARWGGTMITGLDYWGQGTTLIVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYC-----VSGMEYWGQGTSVTVSS 113
                        1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 120;
                                                                                                                                                                                                              APPLICANT: 1
TITLE OF INVENTION: METHODS OF DELIVERING AGENTS TO NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
CITY: Lexington
STRATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.8%; Score 473.5; DB 5 75.0%; Pred. No. 2.6e-40; tive 13; Mismatches 10
                                                                                                                                               Sequence 2, Application PC/TUS9400261
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CBM9:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 991-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 981-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 120 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                           02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                           PCT-US94-00261-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US94-00261-2
                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                      61
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
  à
```

```
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NQKFKGKATLITVDKSSSTAYMQLNSLTSEDSAVYXCAVGGNYVDWFAXWGQGTLVTVSS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NOKFKGRATLITVDKSTSTAYMHLKSLRSEDTAVYYCVSG-----MEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SCHILLBERG, Stefan
APPLICANT: AFRING, Jorg
APPLICANT: Markus
APPLICANT: MONECKE, Michael
APPLICANT: SACK, Markus
APPLICANT: SINGER, Holger
APPLICANT: EMASS, Neil
ITILE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
ITILE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
ITILE OF INVENTION: Resistance
FILE REFERENCE: 014 - 0189P
CURRENT APPLICATION NUMBER: 98 11 9630.6 EP
EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
EARLIER FILING DATE: 1998-10-16
EARLIER FILING DATE: 1998-10-16
SARLIER FILING DATE: 1998-10-16
SARLIER PILING DATE: 1998-10-16
SAFTIER PILING DATE: 1998-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: synthetic, ; OTHER INFORMATION: natural origin US-09-419-788-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.2%; Score 45%; DB 4; Length 267; 75.6%; Pred. No. 2.4e-3%; Live 8; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
40.08-525-539A-78
9.08-08-525-539A-78
9.08-08-08-78
9.08-08-08-78
9.08-08-78
9.08-08-78
9.08-08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.08-78
9.
; Sequence 30, Application US/09419788
; Patent No. 6825325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.61
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

Sequence 3, Application US/09556605;
Patent No. 6417324;
GENERAL INPORMATION:
APPLICANT: Sallberg, Matti
APPLICANT: Lazdina, Una
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
TITLE OF INVENTION: HEAPITITS B VIRUS CORE AND E ANTIGENS:
FILE REPERENCE: TRIEBEP.020A;
CURRENT FILING DATE: 2000-04-21;
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PastSEQ for Windows Version 4.0
SSQ ID NO 3

US-09-556-605-3

```
Sequence 139, Application US/09647468
Fatent No. 6677436
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
TILE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TILLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
TILLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
TILLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 1999-04-02
FRIOR PELICATION NUMBER: DP. 10-91850
FRIOR APPLICATION NUMBER: JP. 10-91850
FRIOR FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSG-----MEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 NQKFKGKATLIYUDKSSSTAFWHLNSLISEDSAVYYCARGGEGYYFDYWGQGTTLITVSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NQKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVS----GMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 NQKFQDKATLIYDKSTSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGTLVTVSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 EVQLVQSGAEVKKPGASVKVSCKASGYSFTGYTMHWYKQSPGMNLEWIGLINPYNGGTVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVOLVOSGAEVEKPGASVKISCKASGSSFTGYNMWWRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVOLVOSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF; OTHER INFORMATION: mouse monoclonal antibody ATR-2
US-09-647-468-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  υ
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 76.1%; Score 451.5; DB 4; Length 118; Best Local Similarity 72.9%; Pred. No. 4.2e-38; Matches 86; Conservative 12; Mismatches 15; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.4%; Score 453; DB 3; Length 136; 75.2%; Pred. No. 3.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
    Patentin Release #1.0, Version #1.30
                CURENT APPLICATION DATA:

CURENT APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-5EP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAM, TYLER
REFERENCE/DOCKET NUMBER: 37,612
RELEFAX: (415) 813-5600
TELEFAX: (415) 849-0792
ITELEFAX: (415) 849-0792
INFORMATION FOR SEO ID NO: 63: SEQUENCE CHARACTERISTICS:
LENGTH: 136 aning acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 75.2%
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-525-539A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-09-647-468-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                    RECOMBINANT PEPTIDES DERIVED FROM THE MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND METHODS OF HUMANIZING ANTIBODY PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVQLVQSGAEVKKPGASVKVSCKASGYSFTGYTMHWVKQSPGMNLEWIGLINPYNGGTVY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVS----GMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NQKFQDKATLTVDKSTSTSTAYMELSSLRSEDTAVYFCARRWRYTMDYWGQGTLVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jequence 63; Application US/08525539A

Sequence 63; Application US/08525539A

Patent No. 6309636

GENERAL INFORMATION:
APPLICANT: DC COUTO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
ITILE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THERE
ITILE OF INVENTION: MC3 ANTI-BA46 ANTIBODY PEPTIDES
ITILE OF INVENTION: MC3 ANTI-BA46 ANTIBODY PEPTIDES
CORRESPONDENCES: 81

CORRESPONDENCE ADDRESS: 81

CORRESPONDENCE ADDRESS: 81

CORRESPONDENCE ADDRESS: 81

CORRESPONDENCE ADDRESS: 82

COUNTRY: USA

STREET: USA

CONTYR: D43

CONTYR: READABLE FORM:
MEDIUM TYPE: RIPM PC Compatible
COMPUTER: READABLE FORM:
COMPUTER: READABLE FORM:
COMPUTER: READABLE FORM:
COMPUTER: TIMP PC COMPATIBLE
COMPATIBLE
COMPUTER: TIMP PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 76.4%; Score 453; DB 3; Length 117; Best Local Similarity 75.2%; Pred. No. 2.9e-38; Matches 88; Conservative 11; Mismatches 14; Indels
        TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY PEE NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSEE: MORRISON & FOERSTER STREET: 755 Page Mill Road CITY: Pala Alto
STRATE: CA
COUNTRY: USA
ZIP: 943-04-1018
COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE FORM: MEDIUM TYPE: Ploppy disk
COMPUTER: LBM PC COMPATIBLE FORM: MEDIUM TYPE: LBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: A24
ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELEPHONE: (415) 494-0792
TELEPHONE: (415) 494-0792
TELEPHONE: GISS SINGLE
TELEPHONE: SINGLE
PETERSON, JERRY A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY:
US-08-525-539A-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-525-539A-63
APPLICANT:
```

g ઠે 셤

```
Gequence 140, Application US/09647468

| Sequence 140, Application US/09647468
| Patent No. 6677436
| GentsAL INFORMATION:
| APPLICANT: SATO, KOH |
| APPLICANT: AABUTA, NAOHIRO
| TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND |
| TITLE OF INVENTION: HUMBER: US/09/647,468
| TITLE OF INVENTION: HUMBER: US/09/647,468
| CURRENT PELING DATE: 2000-09-29 |
| CURRENT PELING DATE: 2000-09-29 |
| PRIOR PILING DATE: 1999-04-02 |
| PRIOR FILING DATE: 1998-04-03 |
| NUMBER OF SEQ ID NOS: 183 |
| SEQ ID NO 140 |
| LENGTH: 118 |
| LENGTH: DATE: DATE OF LENGTH: US OF LEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVOLVOSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVSG-----MEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
| Patent No. 6677436
| GENERAL INFORMATION:
| APPLICANT: SATO, KOH
| APPLICANT: ADACH; HIDEKI
| APPLICANT: YABUTA, NACHINO
| TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) F
| TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMANIZED ANTIBODY
| TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMANIZED ANTIBODY |
| FILE REFERENCE: 05346/0289
| CURRENT APPLICATION NUMBER: US/09/647,468
| CURRENT FILING DATE: 1999-04-02
| PRIOR APPLICATION NUMBER: PT/JP99/01768
| PRIOR FILING DATE: 1999-04-03
| NUMBER OF SEQ ID NOS: 183
| SOFFWARE PATENT OF SEQ ID NOS: 183
| SOFFWARE PATENT OF SEQ ID NOS: 183
| SOFFWARE PATENT OF SEQ ID NOS: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF OTHER INFORMATION: mouse monoclonal antibody ATR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence coding for H chain V region of ant-TF
OTHER INFORMATION: mouse monoclonal antibody ATR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.1%; Score 451.5; DB 4; Length 118; Best Local Similarity 72.9%; Pred. No. 4.2e-38; Matches 86; Conservative 12; Mismatches 15; Indels 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-647-468-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-647-468-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-647-468-140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

76.1%; Score 451.5; DB 4; Length 137;

Query Match

```
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 BIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 79
                                                                           20 BIQLQOSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEMIGYIDPYNGGTIY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSG-----MEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 NQKFKGKATLITVDKSSSTAFWHINSLISEDSAVYYCARGGGGYYFDYWGQGTTLIVSS 137
                                                                                                                           61 NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSG-----MEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: YAMAMOTO, Masato

APPLICANT: YAMAMOTO, HICKO

APPLICANT: YAMAMOTO, HICKO

APPLICANT: YAMAMOTO, HICKO

APPLICANT: TOHDOH, Nacki

TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE

TITLE OF INVENTION: HEPATITIS B CONTAINING THESE

TITLE OF INVENTION: HEPATITIS B CONTAINING THESE

CURRENT APPLICATION NUMBER: US/09/486,814A

CURRENT FILING DATE: 2002-06-13

NUMBER OF SEQ ID NOS: 14
                                                                                                                                               1 EVOLVOSGAEVEKPGASVKISCKASGSSFTGYNMNWVRONIGKSLEWIGAIDPYYGGTSY
                                                      1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                   5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Amino acid;
CTHER INFORMATION: sequence coding for H chain V region of ant-TF;
CTHER INFORMATION: mouse monoclonal antibody ATR-3
US-09-647-468-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.1%; Score 451.5; DB 4; Length 137; 72.9%; Pred. No. 5e-38; tive 12; Mismatches 15; Indels 5
                   Indels
Best Local Similarity 72.9%; Pred. No. 5e-38;
Matches 86; Conservative 12; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09486814A Patent No. 6562599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 86; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-09-486-814A-2
                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            日
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                         g
                                                                                                                                                            g
```

Length 116;

```
Query Match
Best Local Similarity
Matches 85; Conserv
                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                          ð
                                                                                                        셤
                                                                                                                                              ò
                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                           1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                              40 QVKLQESGPELEKPGASVKISCKASGYSFTGYNMKAVKQSNGKSLEWIGYIYPYNGGTGY
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T: Smith, Rodger
T: McCafferty, John
T: Chiswell, David
T: Chiswell, David
T: Pitzgerald, Kevin
T: Fitzgerald, Kevin
T: Kenten, John H.
T: Martin, Mark T.
T: Williams, Richard C.
T: Williams, Richard O.
TINVENTION: Catalytic Antibodies using Phage Technology
                                                                                                                                                                                                                                                                                                                                                                   61 NOKFKGRATLIVDKSTSTAYMHLKSLRSEDTAVYYCVS-GMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                      100 NQKFKSKATLTVDKSSTAYMQLSSLTSEDSAVYCARLGLDYWGQGTTVTVSS 153
                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                     Length 297;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLASSIFICATION: 435
ATTONREY/AGERT INFORMATION:
NAME: REGISTRATION NUMBER: 33,771
REGISTRATION NUMBER: 33,771
RECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                   Query Match 75.8%; Score 449.5; DB 4; Best Local Similarity 75.4%; Pred. No. 1.9e-37; Matches 86; Conservative 12; Mismatches 15;
           ORGANISM: Mus sp., strain; Balb/c, tissue: spleen FEATURE: NAME/KEY: PEPTIDE
                                                                  LOCATION: (1)..(145)
OTHER INFORMATION: Identification Method:
FEATURE:
NAME/EY: PEPTIDE
LOCATION: (177)..(279)
OTHER INFORMATION: Identification Method:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20852
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1530 East Jefferson St. CITY: Rockville STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08273146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 116 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 301-230-0158 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-273-146-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-273-146-55
; Sequence 55, Applicati
; Patent No. 5855885
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                               US-09-486-814A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                   ઠ
                                                                                                                                                                                                                                                                                           ઠે
```

```
1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY 60
                                                                                                                          1 QVQLQQSGPELVKPGASVKVSCKASGYAFTNYNIYWVKQSHGKSLEWIGYIDPYSGGSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDHEMHWVRQAPGQGLEWIGTIDPETGGTAY
                                                                                                                                                                                                  NOKFKGRATLTVDKSTSTAYMHLKSLRSEDTAVYYCVSG---MEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVQLVQSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                              61 NQKFKGKATLITVDKSSSTAYMHLNSLTSEDSAVYYCAGGNPRFAFWGQGTTVTVS 116
                                                     Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NOKFKGRATLIVDKSISIAYMHLKSLRSEDIAVYYC-VSGMBYWGQGISVIVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 NQKFKGRATLTADKSTNTAYMDLSSLRSEDTAVYYCTVLRMDYWGQGTLVTVSS 133
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Raymond John Owens, Martyn Kim Robinson,
TITLE OF INVENTION: Antibodies against E-selectin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 6204007ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٦;
                                                   <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Indels
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,323A
FILING DATE: 11-No. 6204007-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09587526
Patent No. 6407214
GENERAL INFORMATION:
APPLICANT: Raymond John Owens, Martyn Kim Robinson,
TITLE OF INVENTION: Antibodies against E-selectin
NUMBER OF SEQUENCES: 22
75.5%; Score 447.5; DB 2; 73.3%; Pred. No. 1e-37; ive 13; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 447.5; DB :; Pred. No. 1.2e-37 11; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35,719
SR: CARP-0054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08718323A Patent No. 6204007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.5%
Best Local Similarity 76.3%
Matches 87; Conservative
                                                   85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS LENGTH: 133 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΡA
                                                                                                                                                                                                                                                                                                                          RESULT 13
US-08-718-323A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-718-323A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       අ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QVQLVQSGAEVKKPGSSVKVSCKASGYTFTDHEMHWVRQAPGQGLEWIGTIDPETGGTAY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVOLVOSGAEVEKPGASVKISCKASGSSFTGYNMNWVRQNIGKSLEWIGAIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NOKFKGRATLITVDKSTSTAYMHLKSLRSEDTAVYYC-VSGMEYWGQGTSVTVSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 NOKFKGRATLTADKSTNTAYMDLSSLRSEDTAVYYCTVLRMDYWGQGTLVTVSS 133
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6407214ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 57, Application US/07634278
; Sequence 57, Application US/07634278
; Patent No. 553001
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLF, Nicholas F.
APPLICANT: CELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
; NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
; CITY: Palo Alto
CITY: Palo Alto
COUNTRY . California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/587,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 75.5%; Score 447.5; DB 4; Best Local Similarity 76.3%; Pred. No. 1.2e-37; Matches 87; Conservative 11; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PELLING DATE: 11-No. 6407214-1996
ATTORNEY/AGENT INFORMATION:
NAME: TUTJIIO, DOTEON YAKO
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: 37,719
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 133 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                           19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-07-634-278-57
                                                                                               STATE: PACCOUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-587-526-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```